

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCCTCGACCTCGA
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTCGCTCTTCCC
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGTGCCGCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT
GGTGGACAAGTTTAAACAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGCGGGAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCCGCTGCTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGCTGTCTCGCATGC
CAGGCGCGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA
GGCGCAGGGTCTTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGTCATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT
GGACAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACAGTGCGAAGAGTGTGACTCCAGCTGTGTG
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAAC TGCTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCTGACGGCTTCGAAGAAACG
GAAGATGCCGTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT
GCCCTCCCGGAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTAGAAGGATGTCC
CGTGGAAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTCTTGGTTGTTCTTA
AACAGACTTGTATATTTTGATACAGTTCCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCGCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA
TCACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTGCGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTTCTGAGGCGGAAAGAACAGCTGTGGAATG
TGTGTCAATTAGGTGTGGAAGTCCCCAGGCTCCCCAGCAGGCAGAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTTTT

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FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop
><MW: 38192, pI: 4.53, NX(S/T): 2
MRLPRRAALGLLP LLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEKTL SKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWLQLKSEYPDLFEWFVCVTKLVCCSPGTGYPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESKCTCSGLTNRDCGECEVGWVLDE
GACVDVDECAAEP PPSAAQFCCKNANGSYTCCECDSSCVGCTGEGPGNCKECISGYAREHQQCADVDECSLAEKT
CVRKNENCYNTPGSYVCVCPDGFEE TEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

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FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCGCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGCTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTCCCGGCAGCGAGGAGGTCTGAGCAGC**ATG**GCCCGGAGGAGCGCCTTC
CCTGCCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC
CGGGCCCGCCGAGGAGGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA
TAGGATTTGAAGAAGATATCCTGATTGTTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAAATGCCAGCTATTCCTGTCAATATCCATTCCATGAATTTTAC
CTGGCAAGCTGCAGGGCAGGCAGAAATACTTCTATGAATTCTGTCTCTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGAAACAGTGCCTCACAAGGCA
TCAGTTGTTCAAGTTGGTTTTCCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTTGAAGT
GGATGTGATTGTTATGAATTCGAAGGCAACACCATTCTCCAAACACCTCAAATGCTATCT
TCTTTAAAAACATGTCAACAAGCTGAGTGCCACGGCGGGTGCCGAAATGGAGGCTTTTGTAAAT
GAAAGACGCATCTGCGAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTG
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG
GATTTCTATGGAGTGAACCTGTGACAAAGCAAAC**TG**CTCAACCACCTGCTTAAATGGAGGGACC
TGTTTCTACCTTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAAACCTGTGCAAAATGGAGGTAATGCATTGGTAAAAGCAAATGTAAGTGTT
CCAAAGGTTACCAAGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACAT
GGAACTGCCATGAACCCAAACAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGCGCCAGCTCAGGCAGC
ACACGCCTTCACTTAAAAAGGCCGAGGAGCGGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTTAAGTTACACCAAGTTCATAGCCCTTGTAAACCTTTCA
TGTGTTGAATGTTCAAATAATGTTCACTTACACTTAAGAATACTGGCCCTGAATTTTATTAGCT
TCATTATAAATCACTGAGCTGATATTTACTCTTCTTTTAAAGTTTTCTAAGTACGCTCTGTAG
CATGATGGTATAGATTTTCTGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA
TCAGGTTAAAAATTTTCAGTGTGTAGTTGGCAGATATTTCAAATTAACAATGCATTATGGT
GTCTGGGGCAGGGGAACATCAGAAAGGTTAAATGGGCAAAAATGCGTAAAGTCAACAAGAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTCAGATTTTATTGTGAGATATTTAGAT
GTTTGTACATTTTAAAAATTGCTCTTAATTTTAAACTCTCAATACAATATATTTTGACC
TTACCATTATTCAGAGATTCAGTATTAACAAAAAATACTACTGTGGTAGTGGCATT
AAACAATATAATATATCTAAACACAATGAAATAGGGAATATAATGTATGAACTTTTTGCA
TGGCTTGAAGCAATATAATATATTGTAACAAAAACACAGCTCTTACCTAATAAACATTTTAT
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAATAAAAAA
AAAAAATAAAAAAATAAAGGGCGCGCCGCACTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCACTTGTATTGTCAGCTTATAATG

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FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGC
RNGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGSKCKCSKGYQGDLCSKPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERDRP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

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FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTGCGAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG
CCCCAGCCACACCTTCACCAGGGGCCAGGAGGCCACCATGTTGGCGGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCTGGGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCCTCGGCGTGCCACCCCTTTTCCCCGATCCAAGGATGTATGCATGGAGGTCTGTATCTA
TCCAGTCTTGGGAACGTACTGGGACAACGTGAACCGTTGCACCTGCGCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCTTCTGGGGCATGACCTGGATGAGGGGCAATTCGCTACCGCCTGGGACCA
TCCGCCCATCTTCTCGGTCATGAACATGCATGAAATTATACAGTGTCTGAACCCAGGGGAG
GTGCTTCCACAGCCTTCGAGGCTCTTGAGAAGTGGCCCAACCTGATTATGAGCCTCTTGA
CCAAGGCAACTGTGCAGGCTCCTGGGCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATCTCTGGGACATGACGCTGTCTGTGCGCCCGAGAACCTGTCTGTCTTGTGAC
ACCCACAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCTTGCCTCG
CCGAGGGGTGGTGTCTGACCCTGCTACCCCTTCTCGGGCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCC
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCTATACAAGGAGGCATCTACAGCCACACGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC
CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGC CGCGCGCTCAATGAGTGCGACATCGAG
AGCTTGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACTGGGTCACTCAGTGGGCTG
CGGGCACACGCGGGGTCCGGCTGGGATCCAGGCTAAGGGCCGCGGAGAGGGCCCCAATG
GGGCGGTGACCCAGCCTCGCCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT
CCCGCGCGGGTTCCGCTGACGCGAGCGCCCGCTGGGAGCCGCGGGCAGGCGAGACTGGCG
GAGCCCCAGACCTCCAGTGGGGGACGGGGCAGGGCTTGGCTGGGAAGAGCACAGCTGCAG
ATCCAGGGCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTGTAGACAGGGTCTTGCTCCG
TTGCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTCA
AGTGACCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGTGCACACCACACCTGGC
TAATTTTTGTATTTTTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAAC
CTTGGGCTCAAGCGGTCCACTGCTCCGCTCCCAAAGTCTGGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAAA
TAAACCAGGATTTGATAAAAAAAA

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FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCEQDLCCGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPPFPIQGCMMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

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FIGURE 7

AGGCTCCTTGCCCTTTTCCACAGCAAGCTTNTGCNATCCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCCTGGTGGTTCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTCGGGGCAAGCGCCAGGCCACTGCCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACGCCGGCATGGGACCCACTCAG

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FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGTTGCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCTGGTTCTTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCACCTGACCCCTCCCATGGCCCTCTCCAGGACTCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCTCTCTGCTGCTGTTTC
CATGGCCCAGCATTTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACCTCAGGAGGGGCCAGTAAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTCTGTTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

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FIGURE 9

MTHTTTTWARRTSRAVTPTCATPAGPMPCSRLLPSSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMVCTPVPHDPFPMALSRTPTRQISSSDT
DPPADGPSNPLCCCFHGFAPSTLNPVLRHLFPQEAFPAHPIDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

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FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCCTGCTGCCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTAGTACGTAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAAGTACACGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCAGCGGGAAGAGCAAAGACTG
CGTGTTACGGAGATCGTGTGAGAGAACTATACGGCCTTCAGAACGCCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCAGGGCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACACGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGACCAAGCGCACAC
GGCGGCCCCAGCCCCCTACGTTAGTCTGGGAGGCAGGGGCGAGCAGCCCCCTGGGCCGCCTCCC
CACCCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGGCAGATCCCC
GAGGGAGGACCCCTGAGGGCCGCGAAGCATCCGAGCCCCAGCTGGGAAGGGGCAGGCCGGTG
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTGAGCGACTGAAGGCCTTGCGAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTTGTGTTTGTGTTTGTGTTTTCAGGAAAAAGAAAGGGAGAGAGAGGAAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCCTGCACCCACCCCAACTCCCAGCCC
CGGAATAAAACCATTTTCCTGC

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FIGURE 11

MGAARLLPNLTLCQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGABSEKYICMNRGKLIGKPSGKSKDCVFTEIVLE
NNYTAFQONARHEGWFMATFTRQGRPRQASRSRQNRQREAHFIKRLYQGQLFFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

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FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
GACAGCAGCAAGAGGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
CATACGCCCTCAGGAGCTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCTACAGT
CATTTTGATTTTGCTGTTTATTTTCTTTTCTTTTCTTTTCCCACCACATGTGATTTTAT
TTCCGTACTTCAAAATGGGCCCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTTCCCT
GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCCTGCC
CTAGTGTGTGCCGCTGCCACAGGAACTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
CCTCTTGGGATCCCGAGGGGCTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC
TGGATTTTCTGCAGAACTGCACAATGTACAGTGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCCAAGAATGTACAGATTCTCCATTTGCAGGAAAAAC
AATATTCAGACCAATTTACGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCTGTTGGGCTTCTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTTCCAGAA
TCTCAGGAGCTTGCAGCGCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
AGGGCACCTTCAGCCATCTCAAGCTCAAGGAATTTTCAATTGTACGTAAATTCGCTGTCC
CACCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGTCAGGACAACCAGAT
AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCAAACCTGAAGCAGCTC
ACTGCTCGGAATAACCTTGGTTTTGTGACTGCAGTATTAATGGGTACAGAATGGCTCAA
ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCTTGAACAAGTCCGGG
GGATGGCCGT CAGGGAAATTAATATGAATCTTTTGTCTCTGCCACCACGACCCCGGCTG
CCTCTCTT CACCCACGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCTCTCTAT
TCCAAACCTTAGCAGAAGCTACACGCCCTCCAACCTCTACCACATCGAAACTTCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTACCCTGATGGCATA
CAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTT CAGGAGCGCATAG
TCAGCGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTTAGTGCCACTGGATGCTTTAACTACCGCGCGGTAGAAGACACCATTTGTT CAGAGGC
CACCACCATGCCCTCGTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
GTGCTGGTGGTCTTGCTCAGCGTCTTTTGTGGCATATGCACAAAAGGGGCGCTACACCTC
CCAGAAGTGGAAATACAACCGGGGCGGCGGAAAGATGATTATTGTCAGGCGAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAAACAGTTTTCAGATCGTCTCTCTTAAATAACGAT
CAACTCCTTAAAGGAGATTT CAGACTGCAGCCCATTTACACCCCCAAATGGGGGCATTAAATTA
CACAGACTGCCATATGCCCAACAACATGCGATACTGCAACAGCAGCGTGCACAGACTTGAGGC
ACTGCCATACGTAACGCCAGAGGCCACGCGTTATCAAGGCGGAGACATCTTTGAGAA
CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGT
CTATCTTTCTATTTCAAGTTAATTACAAACAGTTTGTACTCTTCTGCTTTTAAATCTT

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FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRNPFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDNDSISTVGVEDGAFREAI SKLLFLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYPSSLNVRGFMCGPEQVRGMARELNMMNLLSCPTTTPGLPLFTP
APSTASPTTPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGERVTPPIISERIQLSIHVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNRYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWYKYNRGRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGGCGGGCGGAGACAGAGGCGAGAGGCAGAAGCTGGGGCTCCGTCTCGCCTCCACGAGCG
 ATCCCAGGAGGAGCGCCGCGCCTCGGCGAGGCGAAGAGGCCAGAGGAAGACCCGGGTGGCTGCGGCCCTTGC
 TCGCTTCCCGAGGCGCCGGGGCTCGAGCCTTGCCTCTTGCTCGCCTTGAAATATGAAAGATGCTCGCAGGCT
 GCCTTTCTGTGATCTCTCGACAGATCTGCTCTCTCCCTGCCAGGCGAGGAGCGGTACAGTGGGAGGTCCATCT
 CTAGGGGCGAGACGCTCGGACCCACCCGAGACGGCCCTTCTGGAGAGTTCCTGTGAGAAACAAGCGGGCGAGACC
 TGGTTTTTCATCAITGACAGCTCTCGCAGTGTCAACACCATGACTATGCAAGGTCAAGAGTTCATCTGTGGACA
 TCTTGCATTTCTTGGACATTTGCTCTGATGTCAACCCAGTGGGCTTGCTCCAATATGGCAGCACTGTCAAGAATG
 AGTTCTCTCCCTCAAGACCTTCAAGAGGGAAGTCCGAGGTGGAGCTGTCTGTCAAGAGGATGCGGCATCTGTCCACGG
 GCACCATGCTGGGCTGGCCATCCAGTATGCCCTGAACATCGCAITTCACAGAGCAGAGGGGGCCGGGCCCTGA
 GGGAGAATGTGCCACGGCTCATATGATCTGTACAGATGGGAGACTTCAGGACTCCGTGGCCAGAGGTGGCTGCTA
 AGGCACGGGACACGGGCTATCTTAATCTTTGCCAITGGGTGGGCGAGGTAGACTTCAACACCTTTGAAGTCCATTG
 GGAATGAGCCCATGAGGACCATGTCTTCCTTGTGGCCAAITTCAGCCAGATTTAGACGCTGACCTCCGTGTTCC
 AGAAGAAGTTGTGCACGGCCCAATGTGCAGCACCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG
 GCTCATACGCTCTGAGGTGCAAAACAGGCTCAITTCCTCAACTCGGATCAGACGACTTGCAGAAATCCAGGATCTGT
 GTGCCATGGAGGACCAACAATGTGAGCAGCTCTGTGTGAATGTGCCGGCTCCTTCTGCTGCGAGTGTACAGTG
 GCTACGCCCTTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAAACAGCGATGTGAAC
 ATGAGTGTGTAATGCTGTATGGCTCTACCTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAATTTG
 CGTGCAACAGGATCAACTACTGTGCATGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT
 ACTACTGCGCGTGCCACCGCTGGCTACACTCTGGAACCCAAATGGCAAAACCTGCAGCCGAGTGGACCATCTGTGCAC
 AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCCTTCTGCTGCGCAGTGTGAGAGGCTTCC
 TCACTCAACGAGGACCTCAAGACCTGCTCCGGGTGGATTACTGCTGTGTGAGTGACCATGGTTGTGAATACTCCT
 GTGTCAACATGGACAGATCCTTTGCTGTGAGTGTCTTGAGGGACACGTGCTCCGAGCGATGGGAAGACGTGTG
 CAAAATTTGAGCTCTTGTGCTCTGGGGGACCAACGGTTGTGAACATTCGTGTGTGAAGCAGTGAAGATTCGTTTGTGT
 GCCAGTGTCTTTGAAGTTATATACTCCGTGAAGATGGAATAAACCCTGCAGAAAGAAAGATGTCTGCCAAGCTATAG
 ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACAGTGCAGAGTGTCTGGAGGGATTCGGGCTCG
 CTGAGGATGGGAAGCTGCCGAAGGAAGGATGTCTGCAATCAACCCACCATGGCTGCGAACACATTTGTGTGTTA
 ATAAATGGGAATTCCTACTCTTCCAAATGCTCAGAGGGATTTGTTCTAGCTGAGGACGGAAGCGGTGCAAGAAAT
 GCACCTGAAGGCCCAATTCGACTTGTCTTTGTGATCGATGGATCCAAGAGTCTTGGGAAGAGAATTTTGAAGTCTG
 TGAAGAGCTTTCTACTTGAATATAGATTCCTTGACAAITTCGCCAAAGCCGCTCGAGTGGGCTGTCTCCAGT
 ATTCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCAGCCAAAGACATGAATAAAGCCGTGGGCC
 ACATGAAATACATGGGAAGGCTCTATGACTGGGCTGGCCCTGAACAACATGTTTGAAGAGTGTTTACCCAAAG
 GAGAGGGGCGAGGCCCTTTCCACAAGGCTGCCAGAGCAGCATTTGTGTTACCGCAGGACGGGCTCAGGATG
 ACGTCTCCGAGTGGGCGAGTAAAGCAAAGCCAAATGGTATCACTATGTATGCTGTGGGATGAGAAAGCAACTTG
 AGGAGAACTACAAGAGATTTGCTCTGAGGCCCAACAAAGCATCTCTCTATCTCGGAAGATTCACGACAAATGG
 ATGAGTAAAGTGAAAACTCAAGAAAGCATCTGTGAACTCTAGAGACTCCGATGGAAGACAGCACTCTCCAG
 CAGGGAGCTGCAAAAAACGGTCCACAGCACAACAGAACTCTGACCGAGTCACCATATAATATCAAGACTTACTTT
 CCGTCTCAATTTTTCAGTGTGCAACACAGATATCTGTTTGAAGAAAGCAATCTTTTACCGCTTACACAAAAGCTT
 CCAATTCACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAAATGTGAAAACCTTATAATGT
 TCCAGAACTTTCGAAACGAGAAGTAAGAAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAAATGGAAGCCC
 TGGAAATCGCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCAITGTATCACGGATTAACAT
 GAACGCGAGTCAGAGGCCCAAAGCTCAGGCTAATGTATAATCAATAATGTGTGTGAAGTAAAAACATCAGTACTGA
 GAAACCTGGTTTGGCCACAGAACAAAGACAGAAGATACACTAATTTGATATAAAATTTATACAGGAAAAAATCCT
 TCAGAATTTCAAGATGAATTTACAGGTGAGAATGAATAAGCTATGCAAGGATTTTGTGAATATACCTGTGGACAC
 AACTTGTCTTCTGCTCATCTCGCTTGTGTGCAATCTCAATTGACTATACGATAAGATTTGCACAGCTTCACTT
 CTGTAGAACACTGGCCATAGGAATGCTGTTTTTTGTACTGGACTTACCTTGATATGTATATGATGATGATG
 CATAAAATCATAGACATCTGACTTGTGGAACAAGTTGGATTTTTTATACAATATAAAATTCACCACTCAG

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FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISGRHARTHPQTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KMRRLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIGVGQVDNFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFPQKKLCTAHMCSSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASNHGCEHECVNADGSYLCQCHEGFALNPDEKTCRINRYCALNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTCRSRVDHCAQQDHGCEQLCLNTEDSFVCQCSGFLI
NEDLKTCSRVDYCLLSDHGCEYSVNMDRSFACQCEGHVLRSDGKTCAKLDSALGDHGCE
HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCCELEGFRLA
EDGKRCRRKDVCSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCCKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQEGGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELQEIASEPTNKHLYAEDFSTMDEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQOPTSESEPTVINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSSHSTKPSGSP
LEKHQCKCENLIMFQNLANEVVRKLTQRLEEMTQRMALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTGAGCGGCTCGGCTCCGCGCACGCTCCGGCCGTGCGCGAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGAATTTCCCTCCCGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACCGGTGTCAG
GCGGTGGAGGGAGGGGAAGTGGTGTTCAGCGTGGTACACCTTGACAGGGGAGGTGTCTTC
ATCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACAGCATTAGATGTGATCCGTG
GGTCTTTAAGCCTCACCAACCTTTGCTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCATGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGTGAGCTGTTGTGGGTACCTGGTTGGACTGGGGTTGCTGGCTGGGTGGTTC
TCTTGTACCACCGCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCTCTGTGACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTCTTCTCTGGCTTGAGCCG
CATGGGTGCTGTGCTGTGATGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTATTGATGAC
CCCACCACTCATTGGCTAAAGGATTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC
CCCCTTGATCTGTACCCCAACCCTATCTAACCAACCCCTGGCTCCCACTCCAGCTCCCTGT
TTATTAAACTAACATGAAATATGTGTTGTTTTATTGCAAAATTTAAATAAAGATACATAA
TGTTTTGTATGAAAAA

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FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVFPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPVHGANTLSCQSFRSKPAVQYQ
WDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL
SSVTSARALRPPHGPFRPGALTPTPSLSSQALPSRPLPTTDGAHPQPISSIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

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FIGURE 18

CGCCACCACCTGCGGCCACCGCCAATGAAACGCCTCCCGCTCCTAGTGGTTTTTTCCACTTTG
TTGAATTGTTCTTATCTCAAAATTGCAACCAAGACACCTTGTCTCCCAAATGC AAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTTCAGGAAATGGTGTACAA
TTTGTAAGATGATAATGAATGTGGAATTTAACTCAGTCTGTGGCGAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGTTTATCATCTAATGTAGAACCCGCTCTGTATAGAAAATGTGAATGCACAACTGCCATT
TAGATAATGTCTGTATAGCTGCAAAATTATTAATAAACTTTAAACAAAATCAGATCCCAATAAAA
GAACCTGTGGCTTTGCTCAAGAAAGTCTATAGAAATTCGTGACAGATCTTTCAACCAACAGA
TATAATTACATATATAGAAAATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACACA
CTATCTCAGCCAAAGGACACCCCTTTCTAACTCAACTCTTACTGAAATTTGTAAAAACCGTGAAT
AATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTTTTGAT
TCATATAACATGAAAACATATTTCATCCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAGCTGCATATGATTTCAAATGGCAATGTTGCAGTTGCATTTTTATATATATA
AGAGATTGGTCTTTGCTTTTCATCATCTGACAACTTCTTATGAAACCTTCAAATTTATGAT
AATTTCTGAAGAGGAGGAAAGAGTCTATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTTATATGAACTTGAAAAATAAACATTTTACATTAAGCTCATCGAAAGGTCACAGATA
GGTATAGGAGTCTATGTGCATTTTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACTCATGCCGTGTAATCACT
GACACATTTTGCAATTTTGATGTCTCTGGTCTTCCATTGGTATTTAAGATTATAAATATTC
TTACAGGGATCACTCAACTAGGAATAAATTTTCACTGATTTGTTCGCCATATGCATTTTT
ACCTTCTGGTTCTTCAGTGAATTTCAAAGCACCAGGACAACAATTCACAAAACTCTTTGCTGT
TAGCCTATTTCTTGCTGAACCTTGTTTTCTTGTGGGATCAATACAAAATACTAATAAGCTCT
TCTGTTCAATCATTGCCGGACTGCTACACTACTTCTTTTTAGCTGCTTTTGCATGGATGTGC
ATTGAAGGCATACATCTCTATCTCATTTGTTGTGGGTGTCATCTACAACAGGGATTTTTGCA
CAAGAAATTTTATATCTTTGGCTATCTAAGCCAGCCGTGGTAGTTGGATTTTCGGCAGCAC
TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAAAACAATTTATT
TGGAGTTTTATAGACACGAGCATGCCTAATCATCTTGTAAATCTTTGGCTTTTGGAGTCAT
CATATACAAAGTTTTTCGTCACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAACA
TAAGGTCTTGTGCAAGAGGAGCCCTCGCTCTTCTGTTCTTCTCGGCACCACCTGGATCTTT
GGGGTTCTCCATGTTGTGCACGCATCAGTGGTTACAGCTTACCTCTTCAGCTCAGCAATGC
TTTCCAGGGGATGTTCAATTTTTTTATCTCTGTGTGTTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTTGTTCAAAAATGTCCCCTGTTGTTTTGGATGTTTAAAGGTAACATAGAGAATG
GTGGATAATTACAACTGCACAAAAATAAAAATTCAGCTGTGGATGACCAATGTATAAAAA
TGACTCATCAAATTATCCAATTATTAACCTACTAGACAAAAAGTATTTAAATCAGTTTTTCT
GTTTATGCTATAGGAACGTAGATAATAAGGTAATAATATGATATCATATAGATATACTATGT
TTTTCTATGTGAAATAGTTCTGTCAAATAAGTATTGTCAGATATTTGGAAGTAATTTGGTTT
CTCAGAGTGATATCACTGCACCCCAAGGAAAGATTTTCTTTTAAACACGAGAAGTATATGAA
TGTCTGGAAGAAACCTCATCTGGCTTGATATTTCTGTGACTCGTGTGCTTTGAAACTAGTCC
CCTACCACCTCGGTAAATGAGCTCCATTACAGAAAGTGGAACTAAGAGAATGAAGGGGCAGA
ATATCAAACAGTGAAAGGGGAATGATAAGATGTATTTTGAATGAACGTGTTTTCTGTAGAC
TAGCTGAGAAATGTTGACATAAAAATAAGAAATGAAGAAACACATTTTACCATTTTTGGA
TTGTTCTGAACTTAAATGTCCACTAAAACAACTTAGACTTCTGTTTGTCTAAATCTGTTTCTT
TTTCTAATATTCTAAAAAAAAGGTTTACCTCCACAATTGAAAAAAA

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FIGURE 19

MKRLPLLVPFSTLLNCSYTNQNTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIEENVNANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESSSSLGYKNNTISAKDTL
SNSTLTETFKVTNNFVQRDTEFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFOKTEFDT
NSTDIALKVFFDSYNNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLPQNYDNSEBEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF
WNYSPTDMNGSWSEGCETYSNETHTSCRCNHLTHFAILMSSGSPSIGIKDYNILTRITQLG
IIISLICLAICITFFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSEIAGL
LHYFFLAAPAWMCIEGHIHLYLVGVVIYNKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYG
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRRHTAGLKEPVSCFENIRSCARGA
LALLFLGLTTWIFGVLVHVVHASVVTAYLFTVSNAFQGMFIPLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

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FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAATATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCACTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

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FIGURE 21

GCTCCCAGCCAAGAACTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCTCTCTCCGCGAGATCCGAACGGCCTGGGCGGGGTCACCCCGGCTGGGA
CAAGAAAGCCGCGCTGCTTGCCTGCCCGGGCCCGGGGAGGGGCTGGGGCTGGGGCCGAGGCGG
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCCGTGGGGCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG
CCGCGCGCGCTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
GGCACTCACAGCCCGCGCAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG
AGCTGCGCCGAGAGCCCGAGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCC
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCTGTGGACTGCGCGCGGGG
CAGAGCGCGCACAGTTTGTGGAGATCAAGGCAGTGCCTCTGCGGACCGTGGCCATCAAGGG
CGTGACACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCCGCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCGAGGAGGCTG
AGGACCTCAGGGGCCACTTGGAAATCTGACATGTTCTCTTCGCCCTTGGAGACCGACAGCATG
GACCCATTTGGGCTTGTCAACGGATGAGAGGCGGTGAGGAGTCCCAGCTTTGAGAAGTAACT
GAGACCATGCCCGGCCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
TGCTTCTACAAGACAGTCTGAGTCCAGTTCGTGTTAGCTTTAGGAAGAAACATCTAGAA
GTTGTACATATTAGAGTTTTCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCCACTGCTGCCTGGGCCCCCATCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTGAATACCTCCATCGATGGGGAAC
TCACCTCCTTTGGAAAAATTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTTAATTTAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAAGTGAAGTGGAGCAGGCATGGCCACCAAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATTTCCC
CTGAGGCCAGTTCTGTGATGGATGCTGTCTGAGAATAACTTGTCTGCCGGTGTCACTGCT
TTCATCTCCCAGCCCACCGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT
CCCAGGCCCCCACCCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAAGAAAGAT
TTGAAGACCCCAAGTCTTGTCAATAAATTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
CCTTTCCCCAGCACTTGGTTTTTCAACATGATATTATGAGTAATTTATTTTGTATATGTACA
TCTCTTATTTTCTTACATATTTATGCCCCCAAATTATATTATGTATGTAAGTGAGGTTTG
TTTTGTATATTAATAATGGAGTTTGTGTTG

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FIGURE 22

MRSGC V V V H V W I L A G L W L A V A G R P L A F S D A G P H V H Y G W G D P I R L R H L Y T S G P H G L S S C F L R I
R A D G V V D C A R G Q S A H S L L E I K A V A L R T V A I K G V H S V R Y L C M G A D G K M Q G L L Q Y S E E D C A F E E
E I R P D G Y N V Y R S E K H R L P V S L S S A K Q R Q L Y K N R G F L P L S H F L P M L P M V P E E P E D L R G H L E S D
M F S S P L E T D S M D P F G L V T G L E A V R S P S F E K

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

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FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGGAAGATGCGGAGGAGAGCCGCCACCGCTCCTCCTGCTG
CTGCTGCGTACCTGGTGGTGCCTTGGGCTATCATAAGGCCATATGGGTTTTCGCCCCAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCAA
AGAAGACTGTTTCTCCAGATTAGAGTGGAAGAACTGGGTCGGAGTGTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAAGGATGGCATCCGTTTGTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAACCTGGAAGT
CTGCAATTTAATACTGTTTCCAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC
TGTTGGATATCGCAGGTGTCTTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCAGCACTTTGGAAGG
CGCGGCGGGCGGATCACGAGGTGAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCC
CATCTCTACTAAAATACAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAAACAGAGCAAGATTCATCTCAAAAATAAAATAAATAAATA
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTCT

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FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLLED
TVTLEVLVAPAVPSCCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST
NSSYTMNTKTGTQLQFNTVSKLDTGEYSCEARN SVGYRRCPGKRMQVDDLNISGI IAAVVVVA
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATMTSENVQWLTPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

090453.21301
106729.254060

FIGURE 25

GACATCGGAGGTTGGGCTAGCACTGAAACTGCCTTTTCAAGACGAGGAAGAGGAGGAGAAAAGAG
AAAGAAGAGGAAGATGTTGGGCAACATTTTATTTAAACATGCCTCCACAGCCCGGACCCCTGGCAT
CATGCTGCTATTCTCTGCAAAATCTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA
ATGAATTACTCAATCTCTCATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAAGAAATAGTAACCTTCTCTTCTCCAATATGTCATGACATTTTGGACAATG
CAATTGTGGCAGCTGGCCTTATTTTCAGTGAAGAAAAAAGCTTTGTGGTTCTATGGCATTTCATCA
TTTGACAAATGCAAGCATCTTCTCTTATCAATCAGCTCCTATTGAACTTACTAGCAGCTGAGCTG
TGGAATCCTTAAAGGGCCATTACATTTCTGAAGAAGAAAAGCTAAAGTGAAGGACATGGCACT
CCGAATTCATGTGCTACTTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAATCAGGCCCTTGGTTTACACCCAGATTCATTTTAT
ATGGAAGCATCTACAGTGGATGTGAATGATTTAGGTCTTTTAACTTTCCAGCCAGATTTGCC
AGCTAACACACAGATTTCTTCTCTACAGACTAACAAATTGCAAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAAATTTATCTTCTAGTCACCAAT
ATTAATGTAAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAAACAACTTACTGA
ACTGCCTGAAAAATGTCTGTCCGAACCTGAGCAACTTACAAGAACTCTATATTAATCAACAAT
TGCTTTCTCAAAATTTCACTGGAGCCTTTATTGGCCTACATAAATCTTCTTCGACTTCACTCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAATCTAGAGAT
TCTGATGATTGGGGAAAAATCCAATTATCAGAATCAAAGACATGAACCTTTAAGCCTCTTATCA
ATCTTTCGAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT
GGACTGGAAAACTTAGAAAGCATCTCTTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTTCAAAAAGTTGTAATCTCAAATTTTGGATCTAAATAAAAATCCTATTAAATAGAA
TAGCAAGGGGTGATTTTAGCAATATGCTACACTTAAAAGAGTTGGGGATAAAATATATGCGCT
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
TACTAACAAACCTTAGATTGTCTTACATTACCCCCAATGCATTTTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCATTTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTATCCGTTG
GATGAACATGAACAAAACCAACATTCGATTCATGGAGCCAGATTCACTGTTTTCGCTGGACC
CACCTGAATTCCAAGGTGAGATGTTCCGGCAAGTGCATTTCAAGGGACATGATGGAAATTTGT
TCTCCTCTTATAGTCTCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT
TTCTTTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAACTCTTGCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACTACTA
GATATAAATGGCGTAACTCCCAAAGAAGGGGGTTTATATACCTTGATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG
GCTCTTTGAATATTTAAATAAGAGATATTCAAGCCAATTCACTTTTGGTGTCTCTGGAAGCA
AGTTCTAAAATTTCTAAATCTAGTGTGTTAAATGGACAGCCTTTGTCAAAGATGAAAAATCTCA
TGCTCGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAAATCTTACTCATCTGAATC
CATCAATCGATATAAAATTTGTATTGATATCCCAACATCTATCAGAAAAACAGAAAAAAA
TGTGTAATGTCAACCACCAAGGTTTGCACCCCTGATCAAAAAGAGTATGAAAAGAATAATAC
CACAACCATTTATGGCCTGTCTTGGAGGCCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCTCAGAAATGAACCTGTGATGGTGGACACAGCTATGTGAGGAATTACTACAG
AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATTAATCTCTGGGAAGCAGGAAA
AGAAAAAGCTACATCACTGAAAGTAAAAGCACTGTTATAGGTTTACCAACAAATATGTCTT
AAAAAACCAAGGAAACCTTCCAAAAATGAAC

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FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNAKIEYSTDFPVNLTGDLSSQNNLSSVTININVKKMPQLLSVYLE
ENKLTLPKCLSELSNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSVIAGINLITEIPDNALVGLLENLESISFYDNRL
IKVPHVALQKVVNLFKFDLKNKPTNRIIRGDFSNMHLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNPNRSLYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSPNIRC
DCVIRWMNMNKTNIRFMEPDLSFCVDPPEFQGGQNVVRQVHFRDMMEICLPPIAPESFPSNINV
EAGSYVSFHCRTAEPQPEIYWIWITPSGQKLLPNTLTDKIFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSPQDNNGSLNLIKIRDIQANSVLVSWKASSKILKSSVKWTAFFV
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

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060710.2254066

FIGURE 27

GCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCAGCAGTGAATCT
GGTAGACCTGTGGTTAACCGGTTCCCTCTCCATGTGTCTCTCTACAAAGTTTGTGTTCTTA
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCTCTGGG
GGTTTAAATGTACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCTCTCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCAC
AACGTGATCTGTAAACGTCCTGTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTACCA
TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATATGTGAGGCAAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTTGCATTGCAGTAGAAATAAGTGGTTACTTCTCCCATCCATTGTAAACATTTGAA
ACTTTGTATTTAGTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTT
AATTTAAAGCAAATAAAAGCTTAACCTTGAAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

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FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMCCKGCLCSSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFLL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

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FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCCATCCTCCTGCTGGTGCT
GGGCTCAGTGCTGTGAGGCTCGGCCACGGGCTGCCCGCCCGCTGCGAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACC GCATCAAAACGCTCAACCAGGACGAGTTCCGCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGGCGCGGTGGAGCCCGGGG
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGCATCAGCGAGAACAAGAT
CGTTATCCTACTGGACTACATGTTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCTACCGCGCCTTCAGCGGCGCTCAACAGCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGCACGGCCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGCTCTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCCAAC
TGCCCTACGCGCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCGGTCCGCCACCTAGTCTATCTCCGCTTCTCAACCTCTCCTACAACCCCATCA
GCACCAATTGAGGGCTCCATGTTGTCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCGAGCTGGCGGTGGTGGAGCCCTATGCCCTTCCGCGGCTCAACTACCTGCGCGTGCTCAA
TGTCTCTGGCAACAGCTGACCACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
AGACACTCATCCTGGACTTCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCCGG
CGCCGCTGCGGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCGCGAGTTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTTCCACTGCCCGCGCG
CCCGCATCCGGGACCGCAAGGCCAGCGAGGTGTTGTGGACAGGGCCACACGGTGCAGTTT
GTGTGCGGGGCGGATGGCGACCCGCGCGCCCATCCTCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGAC
TCCATGCCCGCCACCTGCATGTGCGCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAA
GACCTTCGCTTTCATCTCCAACCGCCGGGCGAGGAGAGGCCAACAGCACCCGCGCCACTG
TGCCTTTCCCTTTCGACATCAAGACCTCATCATCGCCACCCATGGGCTTCACTCTCTTTC
CTGGGCTCGTCTCTTCTGCGCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC
AAAGCACAAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCGAGGCATCAGCTCCGCCG
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCGGGGCGGGGGGCGAGGCCCGG
GGCGGCGGGCAGGGGAAGGGGCTGGTGCACCTGCTCACTCTCCAGTCTTCCCACTC
CTCCCTACCTTCTACACACGTCTCTTTCTCCCTCCGCGCTCCGTCCTGCTGCCCCCGG
CCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCAGACCTGGGGACCCCA
CTACACAGGGGATTGACGACTGGAGTTGAAAGCCGACGACCGACGACGCGCGCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACCTGGGTTTCAATAATTATGGATTTT
TATGAAACTTGAATAATAAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 30

MQVSKRMLAGVSRMPSPLLACWQPIILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLDLDLGNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFLNRLTL
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFQDLNLSLEVGDNDLVYISHRA
FSGNLNLEQLTEKCNLTSIPTALSHLHGLIVLRRLHNLNINAIIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMHLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNLYLRVLNVSGNQLTTLTEESVFHVSNGNLETILDSNPLA
CDCRLLWVFRRRWRLNFNRRQPTCATPEFVQGEKFDKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDDPPAILWLSPRKHLVSAKSNGRLLTVFPDGTLEVRYAQVDNGTYL
CIAANAGGNDMPAHLHVRYSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVFLCLVLLFLWSRGKGNKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

09004532, 071301
T06720, 2250460

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCAGCCCCGGGGATTACGGCTCGCCAGCGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTGCTG
TGTTTCGCTGCTGCTGGGCGCCCGGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCCTGGTGTCTCAAGTGCCAAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCCCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTACAGTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGTCTCAATCTTCACTATGCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGTCTAGGAATTCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCTAAACTGTCACTCTTCTGGGAGCAAG
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCA
ACAGGAAGATCCCAATGGTAAACCTTCACTGTCAAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTTATACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCTCAATGTTAATGACCCAGTCCGGTGCCTT
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGCTG
CTCATCATGTCTCATCTTCTTGGCCACTACTTGATCCGGCACAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTATCTAGAGGCGCTGCCACTTCTCTGC
GCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGACGGGCCGCCCTCCCGCTTGCTCCCAGCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTTGTACTCGGTTTGGAAATGGGAGGGAGGAGGGCGGGGGAGGGGAGGG
TTGCGCTCAGCCCTTTCGCTGGCTTCTCTGCATTGGGTTATTATTATTTTGTAAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
ACAAAAAACA

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FIGURE 32

MGAPAASLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLTYFGEKRALRDNRILQVLTSTPHELSSISISNVALADEGEYTCSTFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLVYPTAMIRPDPPHPREGQ
KLLHCEGRGNPVPFQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVPFLLLIMLIFLGHYILIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAACCCCTTTTCTTCTCCTTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAATTTGTGTCTGTGGCGAGCAGGATGGTTCGCTG
TTACTTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
GCTGGAGACGTCTCTTTGTTTTGCGCTGGAAACGTTACAGGGGACGTTTGCAAGAGAAGA
TCTGTTTCTTGCAATTGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA
AGTCTGCGACGCTTTCACTGCCCCGACTTCCAGTTTACCATTATTTCTGTCATGGCAATTC
CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGG
AAAAAATGGCTTGCATGAAATCGTTCCGGGGCTTTTCTGGTGGTGCATGGTGGTGAAGG
CTGCACATCAACAACAAGATCAAGTCTTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTTAATTATTACGAGATATAGACCCGGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTTACCTGCCAAC
GTGTTCCAGTATGTGCCATCACCCACCTCGACTCCGGGGTAAACAGGCTGAAACCGTGC
CTATGAGGAGGTCTTGGAGCAATCCCTGGTATTGCGGAGATCTGCTAGAGGATAACCCCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAACATTCCTCCAGGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCACCAAGTGCAGGGGTAAAGACCTCAATGAAC
CACCGAACAAGGACTTGTGCTTTGAAACCGAGTGGATTCTAGTCTCCCGGCGCCCTG
CCCAAGAACGAGACTTTGTCTCTGGACCCTGCAACTCTTTTCAAGACAAATGGGCAAGAG
GATCATGCCACACAGGGTCTGCTCCAAACGAGGATACAAAGATCCAGGCACTCGGAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAACCTTAGCTTAACA
GTTTACCCTTGCCCTGGGGGCTGCAGCTGCGACCACATCCCAGGGTTCGGGTTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCGAGGA
GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAAATCGCACTTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACCAACTTTCAAG
AACCCTTTGGCCTCAGGTTGGCTATACATGGATAGCAATTACCTGGACAGCTGTCCCGGGA
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAAACGCTATCCAGCTCA
TCCTCCCGGGCACTTTCAATGCCATGCCCAAACTGAGGATCTCTATTCTCAACAACAACCTG
CTGAGGTCCCTGCCTGTGGACGTGTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA
CAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACAGTTAACTCCATCATCCAGA
TAGACCTCCACGGAACCCCTGGGAGTGCTCCTGCACAATTGTGCTTTCAAGCATGGCGCA
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCTCCCGGTGAACCTCTT
TAGAAGAGATTTCATGCTCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCACGTTAACTTCGCAAGTAAAAACAGCACTGGGTGGCGGAGACCGGACGCACTCC
AACTCTACCTAGACACAGCAGGGGTGTCATCTCGGTGTTGGTCCCGGGACTGCTGCTGTT
GTTTGCACCTCCGCTTCACCGTGGTGGGCATGCTCGTGTATTATCTGAGGAACCGAAAGC
GGTCCAGAGACGAGATGCCAACTCTCCGCGTCCGAGATTAACTCCCTACAGACAGTCTGT
GACTCTTCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCCAACAGAGTGATGACTG
TGGCTCTACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGCGAGGGAAGGCG
ATACATGCTTCCCAACGCGAGGCACCCCGGGGCTGTGAGGGGCTGTACCCAAATCCCGCG
CCATCAGCTGAGTGGGCATAAGTAGATAAATAACTGTGAGCTCGACAACCCGAAGGGCCT
GACCCCTTACTTAGTCTCCTCTTGAACAAGAGCAGACTGGGAGCTGGGAGAGCGCA
GCCAGCTCGCTCTTTGCTGAGAGCCCTTTTGACAGAAAGCCAGACGACCTGCTGGAAG
AATGACAGTGGCCCTCGCCCTCGGCCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAG
CCCCGTGATGGCTCCTGTGGCTACGCAGGGATGGGAGTTGCAGGAAGGCATGAATGTAT
TGTAATAAGTAACCTTTGACTTCTGAC

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FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNVAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNKKIKSFRKQ
TFLGLDDLEYLQADFNLRLRIDPGAQDLNKLEVLILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPIYEEVLEQIPGIAEILLEDNPDWDCTCDLLSLKEWLENI PKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNQEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANS LCPGGCSCDHIPGSGLKMN CNNRNVSSLADLKP
KLSNVQELFLRDN KIHSIRKSHFVDYKNLILDLGNNNIATVENNTFKNL LLDLRWLYMDSNY
LDTLSREKFAGLQNL EYLNVEYNAIQLILPGTFNAMPKLRILILN NNLLRS LPVDVFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHG NFWECSTIVPFKQWAERLGS EVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLVFVTS AFTVVGMLVFLRNKRKSKRRDANSSASEINS LQTVCDDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCCTGACCCAGAACTCAGGGC
TGCACCGGGCCCTGGCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAACTGTTGGC
CGCTGGGCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCGGGGCCCTCAG
AGAAATGAGGCCCGCGTTTCGCCCTGTGCCCTCTTGGCAGGCGCTCTGGCCCGGGCCGGGCGG
CGGCGGAACACCCCACTGCCGACCGTGTGCTGCTCGGCCCTCGGGGGCCTGTCTACAGCGCTC
ACCACGCTACCATTAAGCGGCGAGGCGGCGAGGAGGCTGCATCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCTGCGGGCAGGCCCAGG
GCCCGGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGCATGGAGCGCAGGCGTTCCCACT
GCACCTTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGCTCTCCGACCCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCTGCAACCGCGCGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGGTGCAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCTGCGCCGCGCCCCGGG
GCCGCTCTAACTTGAGCTATCGCGCGCCCTCCAGCTGCACAGCGCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTCTCCTGCCCC
GGGAGGTACCTCCGTGCTGGCAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG
CTTTGCGCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAGGACCGGCCGCTCTTGTGTGACCA
GTGGGGAAGGACAGCCGACCTTGGGGGACCGGGGTGCCACAGGCGCCCGCGGCCACT
GCAACCAGCCCCGTGCCGACAGAAATGGCCAATCAGGGTGCAGGAGAAGCTGGGAGAGAC
ACCACTTGTCCCTGAACAAGACAATTCAGTAACATCTATTCTGAGATTCTCGATGGGGAT
CACAGAGCAGATGTCTACCTTCAAATGTCCTTCAAGCCGAGTCAAAGGCCACTATCAC
CCATCAGGGAGCGTGATTTCAAAGTTAATTCTACGACTTCTCTGCCACTCTCAGGCTTT
CGACTCTCTCTGCGCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGTTGATCT
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTACGAAAGCCCTCTTCCAGCCA
AGGAAGGAGTCTATGGGCCCGCGGGCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC
CAGTTCTGCACATTGCCAAACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCTTGTGCGGAGTCCCCCTTTGGCTCTAGTGATGCAATAGGGAACAGGGGA
CATGGGCACTCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACCTTAC
TTGTGTAACGACAATTTCTGCAGAAATCCCCCTTCTCTAAATTTCCCTTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCTTCCCTGATGATAGAGGAAGTGGAAGTGCTTTAGGA
TGGTGATCTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTCGGAGAA
TTTGGAGAAGTGATGAACTTTTCAAGACATTGGAACAAATAGAACACAATAATAATTACA
TAAAAAATAATTTCTACCAAAATGGAAGGAAATGTTCTATGTTGTTGAGGTAGGAGTAT
ATTGGTTCGAAATCCCAGGGAAAAAATAAAAAATAAAATTAAGGATTGTTGAT

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FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPA RPGA
ASNL SYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIAD EIGARWDKLSG DVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTM TVLGLVKLCFHESPS SQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

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FIGURE 37

CGGACGCGTGGGATTACAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAGTGCCTCCGCCCTGCCGGCCGCGTATC
CCCCGGCTACCTGGGCGCCCGCGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGTGCCGCGCGCGCCGCTGGGGTGCAAACCCCGAGCGTCTACGCTGCC**ATGA**
GGGGCGCGAACGCCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACTGTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTTCTGGAGTGTACCTTCAAATAGCAAATGTACTTGGAAATCA
CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTATAGACCTCGAGAGTGACAAC
CTGTGCCGTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG
CTTCTGTGGCACTTTCGGCCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCGGCTCTTTTAAAC
CCCCAACTGGCCAGACCGGATTACCTTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAAGTTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTTCTTATTCACT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTAGGCCAAAA
AAACTGCCTACAACACAGAGCCTGTACACCAACATTCCCTGTAACCAACGGGTTTAAA
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCAGTGTATCACAAACCATCACTCGCGATGGGAGTTTG
CAGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAATTTGGCGATTACGAGGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTGCTGTGCAAGCAGTGCCCTCTCTCAGAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCCAAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCCTAAAAAATAAGCAATG
T**TAA**CAGTGAACCTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTCT
TCTCAGTAGAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCCTCCGAGATAGCTGAGGGAAGTTCTT
TGCCTGCTCTCAGAGGAGCAGCTATCTGATTGGAACCTGCCGACTTAGTGCGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTTATTATACATCTCTGTAAAAGGAT
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATTATTATAGT
GTTATTTGTTTCACTTCAAGCCTTTGCCCTGAGGTGTTACAATCTGTGCTTGCCTTTCTA
AATCAATGCTTAATAAAATATTTTAAAGGAAAAAAAAAAAA

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FIGURE 38

MRGANAWAPLCLLLAATQLSRQQSPERPVTTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTTFPVTTLGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTTCGCTTCTT
CCTTCTCCGTGGCTACGAGGGTCCCCAGCCTGGGTAAGATGCGCCCATGGCCCCGAAGG
GCCTAGTCCACAGCTGTGCTCTGGGGCTCAGCCTCTTCTCAACCTCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCAGTCTTCTCCCCCGCTCAGCCCCATCCGTGTCATACCTG
CCGGGGACTGGTTGACAGCTTTAACAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG
GTGGAACACTGCCTGGGAGGAAGAGAA'TTGTCCAAATACAAAGACAGTGAGACCCGCCCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCAAGCAGCAGGAGGCCCGGACCTCTTCC
AGTGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGACGGCACCTTCGGGGCCCTCCTGC
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTGGCTTGT
TTTGGCCCCGTGCCCCGATGCTCAGGACCTGAGGAATCAAAGTGTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAAC
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTGCTGTGAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCACCCACGCTGCCCCAGAGCTTGGGCTGCCC
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTGTAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTTGGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTTCACTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAGTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGTCGATGCTGCCAGTTCTCTGT
TCTGTGTTCCACCATCCCCACACCCATTGCCACTTATTTATCTCAGGAAATAAAGA
AAGGCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 40

MAPWPPKGLPAVLWGLSLFLNLP GPIWLQSPSPPPQSSPPPPQHPCHTCRGLVDSFNKGLER
TIRDNPGGGNTAWEENLSKYKDSERLVEVLEGVCSKSDFECHRLLLESEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDQAG
YGGEACGQCGLGYFEARNASHLVCSACFGPCARCSGPPEESNCLQCKKGWALHHLKCV DIDE
CGTEGANCGADQFCVNTESGYECRDCAKACLGC MGAGPGRCKKCS PGYQQVGS KCLD VDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IICALATLAAGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

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FIGURE 41

TGAGACCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCGAGCCCCCTGTGGCTCTGCTGGGCACCTCTGGGTGTTGCCCTTGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT
GCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGAAAGAGGTTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG
AGCCGCTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCGCGCAGCGCCCGGGCC
CGGGTGACCGTTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCTGCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCCAGAGG
GAGCATCTGGGCCCCGTGGCGTCCGGCGCCACAAGCTGGTCCGCTTTGCCTCGCAGGGGGC
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCTGGACCTTGGGGACTATGGAG
CTCAGGGCGACTGTGACCTTGAAGCACAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAAGTGGTGCTGGAGCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTCAAGTGGC
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCTGCCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATAGGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTGTTCTGAAGTGTTGAGGGTACCAGGAGAGCTG
GCGATGACTGAAGTCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT
CCTCTGACAAGTTACCTCACCTAATTTTGTCTTCTCAGGAATGAGAATCTTTGGCCACTGGA
GAGCCCTTGCTCAGTTTTCTCTATTCTATTATTCACTGCACATATATTCTAAGCACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTGCTATTGTTTACTTGTCTGTGCTC
TGGATCTGGGCTAAAGTCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAAAATGAATAAAACATTTTATTCT
AAAA

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FIGURE 42

MQPLWLCWALWVLPASPGAAALTGEQLLGSLLRQLQKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFSQSFREVAGRFLALEASTHLLVFGMEQRLFPNSELVQAVLRLFQEP
VPKAAALHRHGRLSPRSARARVTVEWLRVRDDGSGNRTSLIDSRVSVHESGWKAFDVTAVNF
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSPLPNMRVQKCSASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

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FIGURE 43

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTGTCAGTGGCCTGATCGCGATGGGGACAAA
GGCGCAAGTCGAGAGGAAAATGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCGTGTGGAGTGGAAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGTGTATAATAACAAGATCAAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACCTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCTCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAAGATGGTTCCTCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCTATGTCTCT
GAATCCCAACAGGAGAGCTGGTCTTTGTATCCCTGTGAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTATCTGTGGCAGCCGTCTTGTAAACCCTGATTCTCCTGGGAAT
CTTGGTTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGTGTGAGCCTGGTTCGGCTCACCGCCTATCATCTGCATTTCCTTACT
CAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTTCAAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
ATCTCCTTCATGCCCTCCCTCCCTTTCTTACCCTGCTGAGTGGCCTGGAACCTGTTTAAAG
GTGTTTATTTCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGTGCGAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTCTGCGCTCTTCTCTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGGTCTTCCATCTCTGGGGCCACTCTCTTCTGTCTTCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCTCTCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTGTGGAGAGCATAGTAAATTTTTCAGAGAACTTGAAGCCAAAAG
GATTTAAACCCGCTGCTCTAAGAAAAAGAAAACTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGCGGAGTTTCGGGATCAGCCTGACCA
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

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FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSLAYSGFSSPRVEW
KFDQGDITRLVCYNNKITASYEDRVITFLPTGITPKSVTREDTGYTCMVSEEGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTGMTSNAVRMEAVERNVGVIVAALVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

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FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCCGCCGCGAGCCCGCTTTCCACCCCGACCTCTGCCAGGCCGAGGCCCCAGCTCAG
GCTCGTGCCCAACCACCAAGTTCCAGTGCCGCACCAAGTGGCTTATGCGTGCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCTGCACCGCGGTCA
GTGACTGCTCTGGGGGAAGTGAACAAGAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCTGGAGAGTGTACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTC
CTCTGCGGAGACCAGTCTGGAAGCCCACTGCGCTATGGGGTTATTGCAGCTGTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCAGGAGCGC
CTCCGCCCCTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTGAGAACAGAAGAC
CTCGCTGCCCTTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAAGTGA
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

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FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFCR
TSGLCVPLTWRCRDLDCSDGSDEEECRIEPTQKGQCFFPPGLPCPCTGVSDCSGGTDKKL
RNC SRLACLAGE LRCTLSDDCIPLTWRC DGHPCFDSSDELGCGTNEILPEGDATTMGPPVT
LESVTS LRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTS LP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

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FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAGGAAGTCGATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCCGATTCTACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCTTAGGCTGGATCCCAAGTGA
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTCTATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAACATCTCTGAGC
TCCAGACCTCCTTCCCGTGGGGACTGTGATCTCTATCGCTGCTTTCCCGGATTTAAACTT
GATGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCCACCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGTCT
GCCACCCGCGGCTTGTGAGCGCTACAACCACGGAAGTGTGGTGGAGTTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCTCCTGA
CCACGTGGAAGATGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGTCTGCTGCTCGTCATC
CTGGCCAGGATGTTCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAG
TTCAGCAGTGACCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCCCTACCCGTGGACGACAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA
CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAA
GTTCTGATTACCTCCAGGTGCCAAGAGAGCACCCACCCTGCTTCGGACAACCTTGACATA
ATTGACGACACGGCAGAGGAGTGGCATCCACGAGCCAGGCATCCATCATGCCCACTGGGT
GTTGTTCTTAAGAACTGATTGATTAAAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTTCTCTCTGTTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAATGTCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAGNAAAAA

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FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQPQSPQRL LAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDS
VSGSSELLQSLYSPRCQESTHPASDNPDIIASTAEEVASTSPGIHHAHVLFRLN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

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T02T0.254060

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCCGTGGCCCTAGAGA
TGCTGCTGCCGCGGTTGCAGTTGTGCGCGACGCCTCTGCCCGCCAGCCCGCTCCACCGCCGT
AGCGCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTTCGCTGCTGAGTGCC
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACGAGAACTGATAGAA
AAGTTTCATTGAAAACTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT
CACAAATTAGGAACTGGTATGTGGATGAGCCGTCCTGCGGCAGCGAGGTCTCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGAATGATGA
CCGTGTCAACATGAAGAACAAATTTCAATTGCAATATTTCTGATGAGAAACCAGCAGTTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCAGCATTCCCCCTCTCCTCCTCTGTGGTCAACACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC
TGGCCCTCTCCTCACCGGAAACAGCCCGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATAATTTCAATCCGAGTGTGTT
CGGGAGAAGCCACTCCCAGTGACATGCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAATAAGAAATATATG
GTTATTAGGACATATAAAAACTGAACTGACAACAATGGAAGAAGAAATGATAAGCAAAATC
CTCTTATTTTCTATAAGGAAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGTCTGGCACAATAGTA
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAACACACCTCTGTTTTCTTGTCTCTATACAG
CAGCATATATTATCATACAGACAGAAAAATCCAGAATCTTTCAAAGCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAAAAA

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FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRLGGQPVCRRGTQPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI ESEDEQKLI EKFIENLLPSDGD F WIGLRRREEKQSNSTACQDL
YAWTDGSI SQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPFYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAA NLAYILIPSIPLLLL LV
VTTVCWVWVICRKRKREQDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

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FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGTCTGAAGGGCTGGATGTACGC
ATCCGCGAGGTTCCCGCGGACTTTGGGGGCGCCCGCTGAGCCCCGCGCCCCGAGAAGACTTGT
GTTTGCTCTCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGCGGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCCGAGC
CTGTGTAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAAACCCCGAGCTATTAGAGGTCCACCCCAAACCTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCTGAAGGGGGCATGTTTGTGGGCGAGTGACCAAGGTGGGCAT
GCAGCAAATGTTTGGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCTTTT
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCACATAACATTTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGTGGCTGGGCTTTTCAGTGTGAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTGAGAAGTCTTGATATCCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCATGCTGAAGAGATTTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGATACATACTGCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTGTACCACAAATGGCCACCGTTTGTCT
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT
TCTTGAATGCCATGTGAGTTTATACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCCTTTATACAATG

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FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPILIHTEADSEVLYPNYQSCWSLRQTRGRRQTASLQPGISED LKKVKDRMGIDSSDKVD
FFILLDNVAABEQAHNLPSCPMLKRFRARMIBQRAVDTSLYILPKEDRESLQMAVGPPFLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

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FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTACAGCTCATCACCTTCACCTGCCTTGGTCAATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACACAGACCTGGATTCTTAGCGTCTCCATCTGGAGTGCAGTGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCAGAGAGCTCTTTCTCCCA
GTCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGAAGTGAA
GCACCAGAACAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAGGTGG
TGTGCCCGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCTTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACCTGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGCTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTTCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACATA
CACCATTGTCTCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAGGATAAATTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTTCTGGTAACTTATTACAATAATAAAGATAGCAC
TATGTGTTCAAA

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FIGURE 54

MALLFSLILAICTRPGFLASFSGVRLVGGLHRCGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEEDAGASC
BNPESFSFPVPEGVRLADGPGHCKGRVEVKHQWYTVCTGWSLRAAKVVCRLGCGRVAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGWVGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

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10270-2254060

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTCGGCTGCCTGGG
CGTCTTCGGCCTTTCGGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGCTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGA
TGTGGACAAGAGGGTTCATGGAGACAACTACTTTGGCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTTCGATCAGCATATGCAGCCTCCAAGCAGCAACCCAGGCTTTCCTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTGTCTCACAAAGTGGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACT
AAAACTAGAAATAAACATCTCAAAAGTAAAAAAAAAAAAAAGGCGCGCCGCACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTAC

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FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLCGRNGGAALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQGKMSI
FFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSGRYGVMDDTT
AQGRSPVEVAQDVLAAVGKKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRRKRRKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

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10670-255060

FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAA
GAGGAGAAAATCAGTCACCGCGGAAAATCGTGTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGACTGGGTGCCAAGGTTTCATACCTTTGT
GGTAGACTCGAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA
GGCATTTCCTCCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCCTCGGTCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGTGTTGGA
TTTCATAAACTTTGACAGATGAACCTGGCTGCCCTTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCTAATTTCTGTAAACACTGGCTTCATCAAAATCCAAGTACAAGTTTGGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAGGATCCTTCCTGAGCGTTT
CCTGGCAGTTTTAAACGAAAAATCAGTGTTAAGTTTGTATGAGTTATTGGATATAAAATGA
AAGCGCAATTAAGCACCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCACTTA
ATAGTGCCAGAATTTTAATGTTTGAACCTCTGTTTTTCTAATTATCCCCATTTCTTCAATA
TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCCTTGTCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTTATTAAATAAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
AATTTGTACCATAACCGTTTATTTAACATATATTTTATTTTGTATGCACTTAAATTTTGT
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGATTTTCACAATGAATATCATGAACCTCTAATGGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG
GAGAATTGAGAGAATGTACCCACAATGGCAGCAATAATAAATGATCACACTTAAAAAAA
AA
AA

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FIGURE 58

MKFLLDIILLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDDAIVIGYKMQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

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10270:225626

FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCCGCGGCTC
AGGGAGGAGCACCGACTGCGCCGCAACCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCCCTTTGATGCTGGCCCCGTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAAGGAGACTCAGGACAGCCATTATTCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCGTTCT
TCCCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG
AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCAAGTAACATGA
CCTTGGCTGACAGAGACTTCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAAATCCA
GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTTATACAGTGCACTAATTTCAGTTTTTCAGATATTTCTGAATATAAAAAATA
ATGACTTTTATGTCACTGGGGAGTCTTATGCAGGGAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCTCTGACCAAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAAGTGGTTTGAGGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAAATTTTTTGCGGT
GCACGGAACCTGAGGATCAGCTTACTATGTGAAATTTTTGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAATATAGTTGAAAAGTACTTGGGAGA
AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACCTGGACATCATCGTGGCAGCTGCCTGACAGAGCGCTCCTTGATGGGC
ATGGACTGGAAGGATCCAGGAATACAAGAAGGCAGAAAAAAAGTTTGGAAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGAATCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
TTCATTATGGAAGGATGGGATCCTTATGTTGGATAAACTACCTTCCCAAAAGAGAACAT
CAGAGGTTTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTTTCATATCTGCAAGATTTTTTTCATCAATAAAATTTATCCTTGAAAACAAGTGAGC
TTTTGTTTTTGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTTTAGGGTCTTGAATAGGAAGTTTAAATTTCTTCAAGAGTAAGTGAAAAGTGCAAGTTG
TAAACAAACAAGCTGTAACATCTTTTCTGCCAATAACAGAAAGTTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATATATCCCAATAAATGGATGAAGCTATAA
TAGTTTTTGGGGAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAAATCTTTGAAATA
AAAATATTATATAAAAGTAAAAAATA

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FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGSGQLFLTPYIEAGKIQKGRELSL
VGPFPLNMXSYAGFLT VNKT YNSNLFWFPPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTISNMTLRDRDFPWT T T L S M L Y I D N P V G T G F S F T D D T H G Y A V N E D D V A R D L Y S A L I Q F
FQIFPEYKNND FYVTGESYAGKYVPAIAHLIHSNLPVREV KINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNV TG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLR EDTVQSVKPWLT
EIMNMYKVL IYNGQLDIIVAAALTE RSLMGMDWKG SQEYKKA EKKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWD PYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTGGCTACAACAT
TTTTCCCTTTCTAACAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGCGAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCTGCCTAACAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTGTCTCAATATCAAAATGACTGGCTGGG
TGAACCTTCAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAAGGGCCAGAAA
TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCTGAACATTCTTAAGAGGGAGAAAGTATGTTAAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCCTGGGTC
AGGCCAGCCTCTTTGCTCTCCCGAAATTATTTTGGTCTGACCCTCTGCCCTGTGTTTT
GCAGAATCATGTGAGGGCCAAACGGGGAAGGTGGAGCAGATGAGCACACAGGAGCCGTCT
CCTCACCGCCGCTCTCAGCATGGAACAGAGGCAAGCCCTGGCCCCGGGCTGGAGGTGG
ACAGCCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
ATGCCCTCAGTTGACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT
CCACCAAGGAGCAGGGGGCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCCCTCATCGTGACGCCCTGCAGCGAAGTGCTCACCCTCACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCCTGCTGCGCTGTGGGAGCCTTACCAGGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCTGTGCA
GCCGGAAGCTGCCCGAGACCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCCTGGCCCTGGTCTCCCACTTTGACAT
CTTCTACATCTACGGCTTTGTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCCGAGA
CCCCGTAGGGTGTGGCCATCAACTCCGCTGGAGACCTTTCTACACCTCAGGCATCGTGCGG
CTCTGCAAGGATGACCCCAAGTTCCTCACTCATACGTGTCCTCTGCCCTTCCGGTGCACCCGGGC
CGGGGTGGAATACCGCTCCTGCGAGCTGCTTACCTGGCCAAGCCTGGGACTCACTGGCCC
AGGCCCTTCAATATCACAGCCAGGACGATGTACTTTGGCCATCTTCTCCAAAGGGCAGAAG
CAGTATCACCAACCCGCGGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACT
GCAGATCAAGGAGCGCCTGCAGTCTGCTACAGGGCGAGGGCAACTGGAGCTCAACTGGC
TGCTGGGGAAGGACGTCCAGTGACAGGAAGGCGCTGTCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTTCAACAGGGCTACAGCGTGGTTTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTAGATGCTCCAATGCC
ATTCACTCTCAGCAAAAGACTCTTCTTGGAAAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTTATTTTCTGGGGAACAAGGTTGAATGGGGAGGTAAAGAGGGGTTAAATTTGTG
ACTTAGCTTCTAGCTACTTCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTTCAATATTTCCCAAACCTTTAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAA

FIGURE 62

MGTLGQASLFAPPGNYFWSHSAFCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQFPW
RALEVDRSRVVLLSVVWVLLAPPAAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEDNKSRYPPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL
YQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLRDPRESSAMLDYELHSD FVSSLIKIPSDTLALVSHFDIFYIYG FASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLF AIFSKGQKQYHHPPDDSA LCAFP IRAINLQIKERLQSCYQEGN
LELNWLLGKD VQCTKAPVP IDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLKKVRVYEFRC SNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

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FIGURE 63

AGGCTCCC GCGCGCGCTGAGTGC GGAAGTGGAGTGGGAACCCGGGCTCCC GCGCTTAGAGAAACGCGCATGACCA
 CGTGGAGCCTCCGCGGAGGCGCGCCGCAAGCTGGGACTCCTGCTGCTGCTGCTCTTGGGCTCTCTGGTGCTCC
 GCAGGCTGGAGTGGAGCACCCTGGTGCTCTGCGGCTCCGCGCATCGACAGCTGGGGCTCGAGGCCAAGGGCTGGA
 ACTTTCATGCTGGAGGATTCACCTTCTGGATCTTCGGGGGCTCCATCCACTATTTCCTGCTGCGCCAGGGAGTACT
 GGAGGACCGGCTGCTGAAGATGAAGGCTGTGGCTTGAACACCTCACCACCTATGTTCCGTGGAACTGTGATG
 AGCCAGAAAGAGGCAAAATTGACTTCTCTGGGAACCTGGACCTGGAGGCTCTGCTCCTGATGGCCGCGAGAGATCG
 GGCTGTGGGTGATTCTGCTCCAGGCCCTACATCTGCAGTGAGATGGAACTCGGGGGCTTGCCCACTGGCTGCTAC
 TCCAAGACCTGGCATGAGGCTGAGGACAACTTACAAGGGCTTCACCGAAGCAGTGGACCTTTATTTTGACCAAC
 TGAATGTCAGGGTGGTGCTGCACTCCAGTACAAGCGTGGGGGACCTATCATTTGCCGTGAGGTGGAGAAATGAATAG
 GTTCTTATATAAAGACCCCGCATACATGCCCTACGTCAAGAGGCACTGAGGACCGTGGCATTTGTGGAACTGCT
 TCCGTACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTTGGCCCACTCAACTTGCAGT
 CAACACA CGAGCTGCAGCTACTGACCACTTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGTGAGT
 ACTGGACGGGGTGGTTTGACTCGTGGGGAGGCCCTCACAAATATCTTGGATTCTCTGAGGTTTGGAAAACCGTGT
 CTGCCATTGTGGACGCGCGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATG
 GAGCCATGCACCTTCCATGACTACAAGTCAGATGTACCAGCTATGACTATGATGCTGTGCTGACAGAAGCGGGCG
 ATTACGCGCCCAAGTACATGAAGCTTCGAGACTTCTCGGCTCCATCTCAGGCGATCCCTCTCCCTCCCCACCTG
 ACCTTCTTCCCAAGATGCGGTATGAGCCCTTAAACGCCAGTCTTGTAACCTGTCTCTGTGGGACGCCCTCAAGTACC
 TGGGGGAGCCAACTCAAGTCTGAAAAGCCCATCAACATGGAGAAGCTGCCAGTCAATGGGGGAAATGGACAGTCTCT
 TCGGGTATCATCTCTATGAGACAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG
 TGTTTGTGAACAACAGTATCCATAGGATTTCTGGACTACAAGACAACAGAGATGCTGTCCCCGTGATCCAGGGTT
 ACACCGCTGTGAGGATCTTGGTGGAGAACTCGTGGCGAGTCAACTATGGGGAGAATATTGATGACCAAGCCGAAG
 GCTTAATTGGAATCTCTCATGTAATGATTCACCCCTGAAAACCTTCAGAACTCTATAGCTTGGATATGAAGAAGA
 GCTTCTTTCAGAGGTTCCGCTGGAACAATGGNGTTCCCTCCCAAGAACCCCACTTACCTGCTTCTTCTTGTGG
 GTAGCTTGTGCAGCTCCACGCCCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGGAAGGGGGTGTATTCA
 TCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCCAAGAGACGCTTTACTTCCAGGTCCCTGTGTTGA
 CGAGCGGAATCAACCAGGTCACTGTTTTGAGGAGACGATGGCGGGCCCTGCATTACAGTTTACGGAACCCCCC
 ACCTGGGACGGAACCAAGTACATTAAAGTGAAGCGGTGGCACCCCTCTCTGCTGGTGGCAGTGGGAGACTGCCGCTC
 CTCCTTGAAGCTGAAGCGTGGTGTCTGCCCAACCCCTCACTGCAAAAAGCATCTCTTAAAGTAGCAACCTCAGGG
 ACTGGGGGCTACAGTCTGCCCCCTGTCTCAGCTCAAAACCTTAAGCTCTGAGGGAAGGTGGGATGGCTCTGGGCT
 TGGCTTTGTGTATGATGGCTTTCCTACAGCCCTGCTCTTGTGCGGAGGCTGTGGGCTGTCTCTAGGTTGGGAGC
 AGCTAATCAGATCGCCACGCTTTGGCCCTCAGAAAAAGTGTGAAACGTGCCCTTGCACCGGACGTCACAGCCC
 TGCAGCATCTGTGGAATCAGGCGTGTCTTTGTGTTCTTGGGAGGCTTGGCCACATCCCTCATGGCCCCAT
 TTTATCCCGAAATCCTGGGTGTCTACCAAGTGTAGAGGGTGGGGAAGGGGTGTCTCACTGAGCTGACTTTGTT
 CTTCTTCAACACTCTGAGCCTTCTTGGGATTCTGGAAGGAACTCGGCGTGAGAAACATGTGACTTCCCTT
 TCCCTTCCCATCTGCTGTTCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCTCACCCTGCGTCTTCC
 CAAGTTAGCAGGTGTCTCTGTGTTTCAAGTGGAGGACATGTGAGTCTTGGCAGAAGCCATGGGCCATGTCTGCA
 CATCCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGGCCATGTCTGCACATCC
 AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGGCCATGTCTGCACATCCAGGGA
 GGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGGCCATGTCTGCACATCCAGGGAGGAG
 ACAGAAGGCCAGCTCAGTGGCCCCGCTCCCAACCCCGGACGAGCAGGGGAGAGCAGCCCTCTCTC
 GAAGTGTGTCAGTCTGCAATTTAGCCTTGTCTGGGGCCAGGCCAACACCTGCTTGGGCTCAGTGTCTGTA
 GTTCAGTAAAGCTATAACCTTGAATCAACA

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FIGURE 64

MTTWSLRRRPARTLGLLLLVLGFLVLRRLDWSTLVLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIIHYFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDFSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLP SWLLQDPGMRLRTTYKGFT EAVDLYFDHLSRVVPLQ
YKRGGP IIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKGDL SKGIVQGVLAT
INLQSTHELQLLTFTFLFNVQGTQPKMVM EYWTGWFD SWGGPHNILDSSSEVLKTVSAIVDAGS
SINLYMFHGGTNTFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDY TAKYMKLRDFFGSISGIP
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYE
TSITSSGILSGHVHDRGQVFVNTV SIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYSLDMKKSFFQRFGLDKWXS LPEPTLPAPFLGSL SIS
STPCDTFLKLEGWEKG VVFINQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
 CTGGTGAGGGTTCTCTACTTTGGCCTTCGGTGGGGGTCAAGACGCAAGGACCTACGCCAAAGG
 GGAGCAAAAGCCGGGCTCGGCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
 CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
 AAGAAGCTGTCTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
 GGCAGACACTCGGTCTGTCTAGTGGATAGGGGTATGACCGGTTTCTCTAGACGGGGCCC
 CGTTCCGCTATGTGTCTGGCAGCCTGCACCTACTTTCGGGTACCGGGGTGCTTTGGGCCGAC
 CGGCTTTTGAAGATGCGATGGAGCGGCCCAACGCCATACAGTTTATGTGCCCTGGAACTA
 CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCGGGGACCTCATTGCCTTTCTGA
 ATGAGGCAGCTCTAGCGAACCTGTTGGTCATCTGAGACCAAGGACCTTACATCTGTGCAGAG
 TGGGAGATGGGGGTCTCCCATCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC
 AGATCCAGACTTCTTTGCCGAGTGGACTCCTGGTCAAGGTCTTGCTGCCCAAGATATATC
 CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTAGGTGGAGAAATGAATATGGTAGC
 TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGGCTCTCCGCTGCACTGCTAGG
 AGAAAAGATCTTGTCTCTTACCACAGATGGGCCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
 GACTATATACCACTGTAGATTTTGGGCCAGCTGACAACATGACCAAAATCTTTACCTGCTT
 CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
 CTGGGGCCAGAATCACTCCACACGGTCTGTGTGCTAGCTGTAACCAAGGACTAGAGAACATGC
 TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG
 AATGTTGCCGATAGAAGGGACGCTTCTTCCGATTACTACCAGCTATGACTATGATGCACC
 TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTGGCTCTTCGAGATGTATCAGCAAGT
 TCCAGGAAGTTCCTTTGGGACCTTTACCTCCCCGAGGCCCAAGATGATGCTTGGACCTGTG
 ACTCTGCACCTGGTTGGGCATTACTGGCTTTTCTAGACTTGTCTTGGCCCCGTGGGCCCAT
 TCATTCAATCTTGGCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
 GAACCTATATGACCCATACCATTTTTGAGCCAAACACCACTTCGSGTGCCAAATAATGGAGTC
 CATGACCGTGCCCTATGTGATGGTGGATGGGGTGTTCAGGGTGTGTGGAGCGAAATATGAG
 AGACAAACTATTTTTGACGGGGAAACTGGGGTCCAACTGGATATCTTGGTGGAGAACATGG
 GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG
 GGGCAAAACAATCCTTACCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
 GTGGTTTCCCCCTCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
 ACTCCAAAACATTTCCAATTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
 ACCAAGGGCCAAAGTCTGGATCAATGGGTTTAACTTGGGCCGGTACTGGACAAAAGCAGGGGCC
 ACAACAGACCCCTCTACGTGCCAAGATTCCTGCTGTTTCTTAGGGGAGCCCTCAACAAAATTA
 CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTGGATAAGCCTATC
 CTCAATAGCACTAGTACTTTGCACAGGACACATATCAATCCCTTTCAGCTGATACACTGAG
 TGCTCTGAACCAATGGAGTTAAGTGGGCACCTGAAGGTAGGCGGGGCTGGTGGCTCATGC
 CTGTAATCCAGCACTTTGGGAGGCTGAGACGGTGGATTACTTAGGTCAGGATGCTCAAGA
 CCAGCTTGCCCAACATGGTGAAACCCGCTCTCCACTAAAAATACAAAATTAGCCGGGCGTG
 ATGGTGGGCACTCTAATCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATGCTTGAATCC
 AGGAGGCAGGTTGCGAGTGAGTGGAGGTTGTACCACCTGCACCTCCAGCTGGCTGACAGTGA
 GACACTCCATCTCAAAAAAAAAAAAA

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FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFSYMRLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDGFPADNMTKIF
TLRLKYEHPGLPVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMVMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML
GPVTLHLVGHLLAFDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSGVDTFLYL
PGWTKGQVWINGFNLGRYWTQKGFQQTLYVPRFLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
 ACCCACAAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
 TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTTCAGGATACCTTTGAAGGAATATT
 CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTATAGTGACATTCCAGATGTCAAAAACGATTTT
 GCGTTCTTCTTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTTGGTGTGTT
 CTTGTCAAGAGTTAGTGAATAAACTTAGGGAATTAGTATTGAACCATGAGTGGACATTTG
 AAAAAGCTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTTCATG
 CTGTGCGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
 AATTCCAGAAGCTAAAAATCCTGTCTAAGATTCTCAAAAGACTAACCTCCAAGAGCTCCACC
 TCTGCCACTGCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
 TGCCTTCACGTGAAGTTCATGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAA
 CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAAAATAAGATGATAGGACTTG
 AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCAGTGGAAGAGCAATTTGACCAAAGTT
 CCTTCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTACATAATGACGGCAC
 TAAACTCTTGGTACTGAACAGCCTTAAGAAAAATGATGAATGTGCTGAGCTGGAACCTCAGA
 ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACTGGAT
 TTAAAGTCCAATAACATTGCGACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAAAGACT
 GACTTGTTTAAATTTATGGCATAACAAAATTTGTTACTATTCTCCCTCTATTACCCATGTCA
 AAAACTTGGAGTCATTTATTTCTCTAACACAAGCTCGAATCCTTACCAGTGGCAGTATTT
 AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA
 AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATTCTGC
 CAAAACAATTTGTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAAGCTGCATCACC
 TCACTCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAACCTG
 CTTGGACCGCCTGCCAGCCAGCTGGGCCAGTGTGCGGATGCTCAAGAAAAGCGGGCTTGTG
 TGGAAGATCACCTTTTTTGATACCTGCCACTCGAAGTCAAGAGGCATTGAATCAAGACATA
 AATATTCCTCTTTGCAAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCGGAAC
 AACTTCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
 ATACATCTTTTAAAAATAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
 GTTCAATGTTTGTAGGTTTAAAGTCATTTCAAAATCATTTTTTTTTTTTCTTTTGGGG
 AAAGGGAAGGAAAAATATAATCACTAATCTTGTTCTTTTAAATGTTTGTAACTTGGAT
 GCTGCCGTACTGAATGTTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATGACATT
 TTCTTACTAAAAAATAAAAAAAAAA

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FIGURE 68

MAYMLKKLLISYISIIICVYGFIGLYTLFWLFRIPPLKEYSFEKVVREESSFSDIPDVKNDFAPL
LHMVDQYDQLYSKRFGVFLSEVSENKLRREISLNHEWTFEKLROHISRNAQDKQELHLFMLS
VPDAVFDLTDLVDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPANVYLLKNLRELYLIGNLSENKMMIGLESRLRLHLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAEELQNCLELIPHAIFSLSNLQELDLKS
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESYFSNNKLESPLVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQTQLELKGNCLELDRPLPAQLGQCRMLKKSGLVVEDHLFDLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

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FIGURE 69

CCCACGCGTCGCGCCTCTCTCTGGACTTTGCATTTCCATTCCTTTTCATTGACAAACTGACTTTTTTTATTTCT
 TTTTTTCCATCTCTGGGCGCAGCTTGGGATCCTTAGGCCGCCCTGGGAAGACATTTGGTGTTTTACACACATAGGAT
 CTGTCTTTGGGCTTTCTCTCTCTCCCTGACATTTGGCATTTGCTTAGTGGTTTGGTGGGGAGGGAGACCACTGGT
 GCTCAGTCTTGTCTTCTGCACTTATCTGCTTAGGTACATCGAAGTCTTTGACCTCCATCAGTGATTTATGCTGCTGC
 ATCGCTGGTGTATCTCTGGCGCCCTTGTCTCTGCTGATAGTTTGTCTGCTTGTCTTTACTTCAAATACACAAC
 GCGCTAAAAGCTGCAAGAGAACTTGAAGCTGTGGCTGTAAAAATCAACAACCCAGACAAGGTGTGGTGGGCCAAG
 AACAGCCAGGCCAAAACCATTTGCCACGAGTCTTTGTCTGCCCTGCACTGTCTGTAGGAGTATAGAATGTGTGCC
 AGTTTGTATTTCCCTGCCACCTTGTCTGTGGCAGATAAATGAGGCCCTCTGAGTTAGGAAGGCTCCCTTCTCAA
 GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACTGTTTGTGATGTCCAGGCACAGAAGAAAGGCACAG
 CTCCTCATCAGTTTCATGAAAAATACTCAGTGCCTGCTGGGAACCACTGCTGGAGATCCCTACAGAGAGCTTC
 CACTGGGGGCAACCCCTTCAGGAAGGAGTTGGGGAGAGAGAACCTCCTCAGTGTGGGGAATGCTGATAAACCACTCA
 CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGGCTGGCTGGAACCTGACGTTTCCCTGGAGGTGTCCAGAAA
 GCTGATGTAACACAGAGCCTATAAAAGCTGTGCTCTTAAAGCTGCCAGCGCCTTGCCAAAATGGAGCTTGTA
 AGAAGGCTCATGCCATTGACCTCTTAATTCTCTCTGTTTGGCGGAGCTGACAAATGGCGGAGGCTGAAGGCAAT
 GCAAGCTGCACAGTCAGTCTTAGGGGTGCCAATATGGCAGAGACCCACAAGCCATGATCCTGCAACTCAATCCC
 AGTGAGAAGCTGCACCTGGCAATAGAAAGACAGAAAAACAAAGCATCAGAAATATCTTTTCTTATGTCCAGCTT
 GATCCAGATGGAAGCTGTGAAAGTGAAACATTAAAGTCTTTGACGGAACTCCAGCAATGGGGCTCTGCTAGGG
 CAAGTCTGCAGTAAAAAGCATATGTTCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT
 GACTCAGCAAGAAATCAAAGAACTGTCTTTGTCTTCTACTACTTCTCTCTCTCCTTAACATCTCTATTCCAAAGTGT
 GGGCGTTTACCTGGATACCTTGGAGAGATCCTTACCAGGCCCAATTACCCAAAGCCGATCTCTGAGCTGGCTTAT
 TGTGTGTGGCACATTAAGTTGGAGAAAGATTACAAGATAAACTAAACTTCAAAGAGATTTTCTTAGAAATAGAC
 AAACAGTGCAATTTGATTTTCTGCCATCTATGATGGCCCCCTCCACCACTCTGGCCTGATGGACAAGTCTGT
 GGGCGTGTGATCCCACTTCTGAATCGTCAACAACTCTGACTGTGCTGTGTCTACAGATTATGCCAATCT
 TACCGGGGATTTCTGCTTCTTCAACCTCAATTTATGAGAAAAACATCAACATCATCTTTAACTTGTCTCTCT
 GACAGGATGAGAGTTTATTAAGCAAATCTACCTTAGAGGCTTTTAACTCTAATGGGAATAACTTGAAGTATCAAC
 GACCCAATTTGCAGACCAAAATATCAAATGTTGTGGAAATTTTCTGCTCCCTTAAATGATGTGGTACAATCAGA
 AAGGTAGAAGATCAGTCAATTTACTTACAACCAATAATCACTTTTCTGACTCTCAACTTCTGAAGTATCAAC
 CGTCAGAAACAACTCAGATTATTGTGAAATGTGAAATGGGACATAATTTCACTGAGGAGATATATACATAACA
 GAGATGATGTAATACAAAGTCAAAATGCACTGGGCAATATAACACACAGATGGCTCTTTTGAATCCAAATCA
 TTTGAAAAGACTATATTGAATACCAATATATAGTGGATTTGAACCAACTCTTTTGTTCAGGTAGTCTGCAC
 ACCTCAGATCCAAATTTGGTGGTGTCTTGTATACCTGTAGAGCTTCTCCAACCTCTGACTTTGCATCTCCAAC
 TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAACTTTGTAAGGTGTATCCCTTATTTGGACATATGGGAGA
 TTCCAGTTTAAATGCTTTAAATCTTGTAGAAATGAGCTCTGTGTATCTCAGTGTAAAGTTTGTATGTGTAT
 AGCAGTGACCACAGTCTCGTGCATCAAGGTTGTGCTCCAGAAGCAACGAGAACTTTCTCATATAAATGG
 AAAACAGATTTCCATCATAGGACCACTTCTGCTGAAAAGGGATCGAAGTGCAGTGGCAATTCAGGATTTCCAGCAT
 GAAACACATGCGGAAGAACTCCAAACCAAGCTTTCAACAGTGTGCATCTGTTTCTTCCATGTTCTAGCTCTG
 AATGTGTGATCTGAGCGACATCAGTGTAGGCAATTTGTAAATCAACGGGCAGACTCAAATACCAAGAGCTG
 CAGAACTATTAACAAAGTCCAAACCTAAGTGAGACATGTTTCTCAGGATGCCAAAGGAAATGCTACCTCGT
 GGCTACACATATTAATGAATTAATGAGGAAGGGCTGAAAGTGACACAGAGCCCTGCATGTAAAAAA

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FIGURE 70

MELVRRMLPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIIFSIVQLDPDGSCSENIKVFDGTSSNGPLLGQVCSKNDYVVPFESSSSSTLT
FQIVTDSARIQRTVFVFYFFSPNISIPNCGGYLDTLEGSPTSPNYPKPHELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIIVKCEMGHNST
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPPYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDPASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDIIGPIRLKRDRSASGNSGFGHETHA
EETPNQPFNSVHLFSFMVLALNVVTIVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
 GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGTC
 TGCTGCCCGCCGCCCGTGCCTGCCACAGCGCCACGCGCTTCGACCCCACTGGGAGTCC
 CTGGACGCCCCGCAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG
 GGGAGTGTTTTCCGTGCCAGCTTCGGTAGCGAGTGTTCTGGTGGTATTGGCAAAAGGAAA
 AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCTCCTAGTTTCAAATATGAAGAT
 TTTGGACCACTATTTACAGCAAAATTTTTTAAATGCCAACAGTGGGCAGATATTTTTCAGGC
 CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT
 CAGAATATTCTGGAACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
 CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGCTTTTGACTGTACTATTCCCTTTTTGA
 ATGTTTTCATCCGCTCTTCTTGGAGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG
 TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG
 TCGGATGTTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT
 ATATAATGAAAGCCAGTTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
 TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
 CATAAATGGGAAAACCTGCATGACAATAGACAACTGTCTGGGGCTATAGGAGGGAAGCTGG
 AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTTTCATGTG
 GAGGAAATCTTTTGATGAATATTGGGCCCACACTAGATGGCACCATTCTGTAGTTTTTGAG
 GAGCGACTGAGGCAGGTGGGGTCTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA
 TACCTGGCGATCCCAGAATGACACTGTACCCCAAGATGTGTGGTACACATCCAAGCCTAAAG
 AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCTTGGCCAT
 CCCAAAGCTATTTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG
 GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC
 CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
 ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA
 AAGCAATGTAACCTGGATAAGAAAAATTATTTGGCAGTTTCAGCCCTTTCCTTTTCCCACTA
 AATTTTTCTTAAATTACCCATGTAACCATTTTAACTCTCCAGTGCACTTTGCCATTAAAGTC
 TCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTTCACATTATAGTAG
 CAAGGAATTGGTGGTATTATGGACCGAACTGAAAAATTTATGTTGAAGCCATATCCCCCATG
 ATTATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAAT
 TTTTTTTTGTGCCAACATCATAGAGTGATTTACAAAAATCTAGATGGCATAGCCTACTACA
 CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
 AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAACATAGAGAAG
 GTACAGTAAAAATACTGTAAAAATAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG
 CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCTAGGACATTA
 TTGAACACTGCCAGCGTTATAAAATCTGTATGCTTAGGCTACACTACATTATATAAAAAAA
 GTTTTTCTTTCTTCAATTATAAATTAACATAAGTGTACTGTAACTTTACAAACGTTTTAATT
 TTTAAACCTTTTGGCTCTTTGTAATAACACTTAGCTTAAACATAAACTCATTTGTGCAA
 ATGTAA

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FIGURE 72

MRPQELPRLAFPLLLLLLLLLPPPPCPAHSATRFDPFTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRDRLRFGLYYSLEW
FHPFLPEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGNNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVPDQVWYTSKPEKEKLVYAIFLKWPTSGQLFLGHGPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

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TOTY 0.234060

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTTGAGCATCTGCCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT
TTCCATCCAGGTGTCTGACAGAATTATGGGGATCACCTTGTGAGCAAAAGGCGAACCAGC
AGCTGAATTTACAGAAGCTTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGAGCTATGGCTGGGTGGGAGA
TGGATTCTGGGTCTCTCTAGGATTAGCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCTGATTTGGGAAGGTTCCAGTGAGCCGACAGTTTGACGCTAATGTTTACAACTCATCTGAT
ACTTGGACTAACTCGTGCAATTCAGAAATATCACCAACCAAGATCCCATTATTCAACACTCA
AACTGCAACACAAACACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCTT
ACTCTACAATACCTGCCCTTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAATTGATTTGTGTACAGAAGTTTTTATGGAAACTAGCACCATTGTCTACAGAAAC
TGAACCAATTTGTTGAAAATAAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTTGCTCTCCTCTTCTTTGGTGTGTCAGCTGGTCTTGGATTTTGC
TATGTCAAAAGGTATGTGAAGGCCCTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGA
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCTGGAA
GCTGAAGTTT**TAGAT**GAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCC
TTACCTTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCTT
GGTTCCTAACTGGAATCAGCTCAGGACTGCCATGGACTATGGAGTGCACCAAGAGAAATGC
CCTTCTCCTTATTGTAACCCGTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCAGGGCC
TTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGCAAAGTGCAA
GGACCTAAAACATCTCATAGTATCCAGTGGTAAAAAGGCCCTCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGAC
CCTTTCTTCACTCTGAAAGAGAAAAACGATATCCCACTGACATGTCTTCTGAGCCCGGT
AGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAGCTAAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTTCTGTAACAATTGAGTTGGA
ATCACTGTTTAGAACACACACTTACTTTTCTGGTCTCTACCACCTGCTGATATTTTCTCT
AGGAAATATACTTTTACAAGTAACAAAAATAAAACCTTTATAAATTTCTATTTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTC
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATCTCTCAAAAAATTGCATAGTAGAAGCGCTATCTGGGAAGCTATTTTTTCA
GTTTTGATATTTCTAGCTTTTACTTCTTCCAACTAAATTTTTATTTTTGTCTGAGACTAATCTT
ATTCAATTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAACTACCTAAGAAG
TACATTGTTACCTCTATATACCAAGCACATTTTAAAAGTGCCATTAAACAAATGTATCACTA
GCCCTCCTTTTCCAAACAAGAAGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA
AGCATTTAGAAAACCTT

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FIGURE 74

MARCFSLVLLLTISIWTRRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGLIWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

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FIGURE 75

AGATGCGGGTCTTGGCACCTCTAATTGCTCTCGTGTATTTCGGTGCCGCGACTTTACGATGG
CTCGCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGCTGCCTTCTTACTCGTGAGGAA
ACTGCCGCGCTCTGCCAGGTCTGCCACCCCAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT
TCTTTTCTTCGCTTGGATATTGCGATGGGCCTACTTTACATCACACTCTGCGATAGTGTTC
TGATGACGTGCAAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAAC TAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCCTTTGCCAA
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAC
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGCTCATGGACCTTCTCTG
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGA
TGGGGAAAACAAGAAGGATAAA TAAGATCCTCACTTTGGCAGTGCTTCCTCTCTGTCAATT
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGG
CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG
GCACCCTACAGGAAGGCCTGCCATGCTGTGGCCAAC TGTTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAATGTTTTCCCTCCAAGCTTGGGTGAGTGTGTTAACTGCTTATC
AGCTATTCAGACATCTCCATGGTTTTCTCCATGAAACTCTGTGGTTTTATCATTCCTTCTTAG
TTGACCTGCACAGCTTGTTTAGACCTAGATTTAAACCCTAAGGTAAGATGCTGGGGTATAGAA
CGCTAAGAATTTTCCCCAAGGACTCTTGCTTCTTAAAGCCCTTCTGGCTTCGTTTATGGTC
TTCATTTAAAGTATAAGCCTAACTTTGTGCTAGTCTTAAGGAGAAACCTTTAACCACAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCTGGACTTTCAC
TAACCTCTGACATACTCCCCACACCCAGTTGATGGCTTTCGGTAATAAAAGATTGGGATT
TCCTTTTG

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FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGHNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYN
TGLNFGKVDVGRYTDVSTRYKVSTSP LTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

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FIGURE 77

GGACAGCTCGCGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTTGCCCTG
GGGCCCCAGCTGGCCCCGGGTACCCCTGGCATGAGGAGATGGGCCCTGTTGCTCCTGGTCCCA
TTGCTCCTGCTGCCCGGTCTTACGACTGCCCTTCTACAACGGCTTCTACTACTCCAACAG
CGCCAAACGACCAGAACCTTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCTGTTTACCTACCAAGGGGGCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGGCGTGTGCGTGTCAAATGGTGGAGCT
GTGGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT
TTGGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCAATTGACGGGCTGGA
GGATGAAAGCGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTTCTTACCAGTCCCCCA
ACGGGCGCTACCACTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTG
GTGGCTCCTTTGAGCAGCTCTTCCGGGCTGGGAGGAGGGCTGGACTGTGCAACGCGGG
CTGGCTGACAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCCGCGCAGCCCTGCGGTGGCC
CAGGCTTGGCACCTGGCGTGCAGAGCTACGGCCCCCGCCACCGCCGCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGGCGGGTGTACTACCTGGAGCACCCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCTGCCAGGAAGATGATGCCACGATCGCCAAAGTGGGAC
AGCTCTTTGCCCGCTGGAAGTTCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCTGTGGTTCACCCGCATCCTAACTGTGGGCCCCAGAGCCTGGGT
CCGAAGCTTTGGCTTCCCCGACCCGAGAGCCGCTTGTACGGTGTTTACTGCTACCGCCAGC
ACTAGGACCTGGGGCCCTCCCCGCGCATTCCTTCACTGGCTGTGTATTATTAGTGGTT
CGTTTTCCCTTGTGGGTGGAGCCATTTTAACTGTTTTTATACTTCTCAATTTAAATTTTCT
TTAAACATTTTTTTACTATTTTTTGTAAAGCAAACAGAACCCAATGCCCTCCCTTTGCTCCTG
GATGCCCCACTCCAGGAATCATGCTTGCTCCCCGCGGCAATTTGCGGTTTTGTGGGCTTCTG
GAGGGTTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGGCCAGAGTGGGC
GGTGGCCTGTCTAGAATGCCGCGGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCCCTT
CAGCCTGGGGGAAGAAGAGGGCCTCGGGGGCTCCGGAGCTGGGCTTTGGGCTTCTCCTGCC
CACCTTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAACTCCCTCCCCGTTCCCTT
TCCCTTCTCGTTCCAAAGAATCTGTTTTGTTGTCAATTGTTTCTCCTGTTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTGTAATTTGGACAATAAATGGTGTATGACTGCCTTCCGCCAA
AA
AA

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FIGURE 78

MGLLLLVLPLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLLHRYDVF CFATALKGRVYYLEHPEKLTITEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYFVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

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FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC
TTCTGTGTCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCGGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA
CTTCCAGTACGACCATGAGGCTTTCTTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGCTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGGAC
GGCGACGGCTGGGTGTCTGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA
CATACGGGACTCGGTGAGCGCGGCCTGGGACACGTAACGACACGGACCGCGACGGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCGGTGAAGAATTTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGGCGTTTCCGGGTGGC
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCTGCAACCCGAGG
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCCGGGACTTCCGGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCTTGCCAGGACCAGCCC
CTGGTGAAGCCAACCACTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA
AGCGGAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCACGATGAGCTGTGAGACACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGGCCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCGCAGGAG
GCAGATGCAGTCCCAGGCATCCTCTGCCCTGGGCTCTCAGGACCCCCCTGGGTGCGCTTC
TGTCCTGTGCACCCCCAACCCAGGGAGGGGCTGTCTAGTCCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGCCCCAGACCCAGGGACCTTGGCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCTT
GGCCCCAGCCCTCTCCTGCCTGGCCTGGCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

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FIGURE 80

MMWRPSVLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTRDGRVGEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFILHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPANVQTERQQ
FRDFRDLNKDGHLDGSEVGHWWLPPAQDQPLVEANHLHESDTRDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGGCCCGG
 CGGGCGGGCCGGGTGCGAGGGATCCCTGACGCCCTCTGTCCCTGTTTCTTTGTGCGCTCCAG
 CCTGTCTGTGCTCGTTTGGCGCCCCCGCCTCCCGCGGTGCGGGGTGCAACCGATCCTG
 GGCTTCGCTCGATTGCGCGCGAGGCCCTCCAGACCTAGAGGGGCGCTGGCCCTGGAGCAG
 CGGGTCGTCTGTGTCCTCTCTCCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGCGGGGCTCT
 GAGGAGGTGACGCCGGGGGCCCTCCCGCACCTGGCCTTGCCCGCATTCTCCCTCTCTCCGAG
 GTGTGAGCAGCCTATCAGTCACCAATGTCGCGAGCCTGGATCCCGGCTCTCGGCCCTCGGTGTG
 TGTCTGCTGCTGCTGCCGGGGCCCGGGGAGCGAGGGAGCCGCTCCATTGCTATCACATG
 TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCACGGGGGCTGCC
 CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
 GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGCTATAGCCCTACC
 TGGTCGAGAAAACTATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAAATGCTTCTAGAT
 GGTCTGCTCTTTTACAGTAACATAAGGCCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
 GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAAACCCCGAGAAGAAAACTGG
 CAATAAAGATTGTAAAGCAGACATTGCATTCTGTATTGATGGAAGCTTTAATATTGGGCAGC
 GCCGATTTAATTTACAGAAGAAATTTGTTGGAAAAAGTGGCTCTAATGTTGGGAATTGGAACA
 GAAGGACCACATGTGGGCTTGTTCAGCCAGTGAACATCCCAAAATAGAAATTTTACTTGAA
 AAACTTTACATCAGCCAAGATGTTTTGTTTGGCCATAAAGGAAGTAGGTTTTCAGAGGGGGTA
 ATTCGAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATCTTTCACGCTAGATGCTGGA
 GTAAGAAAAGGGATCCCAAGTGTGGTGGTATTATTATGATGGTTGGCCCTTCTGATGACAT
 CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTATAGTTTCTGTGGCCA
 AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTCACATTGTTGACAAGGCTGTCTGT
 CGGAATAATGGCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAA
 GCCTCTGTGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCGAGCAAGCTGTATAAAT
 CAGTGAACATTGCTTCTAATTGATGGCTCCAGCAGTGTGAGATAGCAATTTCCGCCTC
 ATGCTTGAAATTTGTTTCCAACATAGCCAAGACTTTTGAATCTCGGACATTGGTGCCAAAGT
 AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCAGTTTCACTGACTATAGCACCA
 AAGAGAATGTCTAGCTGTCTCAGAAACATCCGCTATATGAGTGTGGAACAGCTACTGGT
 GATGCCATTTCTTCACTGTTAGAAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAGAA
 CTTCTTAGTAATTTGTACAGATGGGCAGTCTATGATGATGTCCAAGGCCCTGCAGCTGTG
 CACATGATGAGCAAGTAACACTACTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG
 AAAGATATGGCTTCTAAACCGAAGAGTCTCAGCCTTCTTCAAGAGAGTTTCACAGGATT
 AGAACCAATTTGTTTCTGATGTCTCAGAGGCATTGTAGAGATTCTTAGAATCCACAGCAAT
 AATGGTAACATTTTGACAACTGAAAGAAAAGTACAAGGGGATCCAGTGTGTAAATTTGTATT
 CTCATAATACCTGAATGCTTTAGCATAGTAATCAGATACAAAACCTATTAAAGTATGTCAAC
 AGCCATTTAGGCAATAAGCACTCCTTTAAAGCCGCTGCCTCTGTTTACAAATTTACAGTGT
 ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAAACCTCAGGAAAGAGGA
 GATAATGTGGATTAAAAACCTTAAGAGTTCTAACCATGCCCTACTAAATGTACAGATATGCAAA
 TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAAAA

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FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEFVSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFALKEVGFRRGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCHEQMMCSKTCYNSVNI AFLI
DGSSSVGDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHADAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

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FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCGCCACCGCGCGCTCCCGCATCTGCACCCGAGCC
GGCGGCTCCCGCGGGAGCGAGCAGATCCAGTCCGCGCCGAGCGCAACTCGGTCCAGTCG
GGCGCGCGCTGCGGGCGCAGAGCGGAGATGCAGCGCTTGGGGCCACCTGCTGTGCTGC
TGCTGGCGGCGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCAGCTCGGCTCCAGTC
AAGCCCGGCGCGCTCTCAGCTACCCGAGGAGGAGCCACCTCAATGAGATGTTCCGCGA
GGTTGAGGAACCTGATGGAGGACACGACGACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTAT
CACAATGAGACCAACACAGACACGAAGGTTGGAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACACAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCATCATCTG
TGGGAGACGAAGAGGACAGAAGGAGCCACAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTACTGCCAGTTTGGCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACAAAA
TGGCCACCGAGGGGACGAATGGGACCATTGTGTGACACACGAGGGAGTGCACGCCGGGGCTG
TGCTGTGCCCTTCCAGAGAGGCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA
GCTTTGCCATGACCCCGCCAGCGGCTTCTGGACCTCATCAGTGGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGTGCC
CAGAGAGGTCCTCCGATGAGTATGAAGTTGGCAGCTTATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGTGGGGAGCCTGCGGCTGCCGCGCTG
GCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA
ATAGCTAATTTATTTCCACAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCTCTACA
TCTTCTTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCAGC
TCCCCAGGCTGTTCTCCAGGCTTCAAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAAC
TGCAGGAGCAGTTTGCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAG
ACAGCCGTTTGTCTACATGGCTTTGATAATTGTTTGGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTCTGATTTGGTTTGGGGAAATGTGGAGAAGAGTGCCTGCTTTGCAACATCAA
CCTGGCAAAATGCAACAAATGAATTTTCCACGAGTCTTTCCATGGGCATAGGTAAGCTG
TGCTTTCAGCTGTTGCAGATGAAATGTTCTGTTTCAACCTGCATTACATGTGTTTATTTCATCC
AGCAGTGTTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC
CCTCTCTCAGCACAGCCTGGGGAGGGGGTCAATTGTTCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCCACACAGCTAGTGAAGACCAGAGCAGTTTCAT
CTGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACAGCCCTTGGTGCCACCAA
AAGTGTCTCCCAAGGAAGGAGAATGGGATTTTTCTTGGAGCATGCACATCTGGAATTAAG
GTCAAACATAATTCACATCCTCTTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGCGAGCGCTCCTTCTAATGAAGACAAATGATATGACACTGTCCCTCTTTGGCAGT
TGCATTAGTAACTTTGAAGGTATATGACTGAGCGTAGCATACAGGTTAACTCGCAGAAACA
GTACTTAGGTAATGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC
TGAAGACATTAACAACACGTGGAGAAAATCAAACGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCAGCTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTCAGGTGTGA
TGGACTGTTGGCCACTGTATTTCATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGTGTA
TAAGCATGCTTTCTTTGAGTTTAAATTTATGTATAAACATAAGTTGCATTAGAAATCAAGC
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRDSECCG
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

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100170225090

FIGURE 85

AAGGAGGCTGGGAGGAAAGAGGTTAAGAAAGTTAGAGAACTTCACTCATCTCTCTGGGCTCAGAAGGACTCTG
 AAGATAACAATAATTTTCAGCCCATCCACTCTCTCTCCCTCCCAACACACATGTGCATGTGACACACATACAC
 CACACATACACCTTCTCTCTCTCACTAGAGACTTCACAGTCACTCACTCTGTGAGCAGGTTCATAGAAAGGACAC
 TAAAGCCTTAAAGGACAGCCCTGGCCATTACCTCTGCAGTCTCTTGGCTTGTGAGTCAAAAACATCCGGAGGG
 CCAGGCACGGTGACTCACTCACTCTGTAATCCAGCACTTTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTCAAGAG
 TTCCAGAGCAGGCTGGCCACATGAGAGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGAGTGGTGGC
 AGGTGCCTGTAATCCAGCTACTCAGGTGGCTGAGCCAGGAGAAATCGTTGAATCCAGGAGGCGGAGGATGCAGT
 CAGCTGAGTGCACCGCTGCACTCCAGCCTGGGTGACAGAAATGAGACTCTGTCTCAAAACAAACAAACACGGGAGGA
 GGGGTAGATGACTGCTTCTCTGCAACCTCTTAACTCTGCATCTCTTCTTCCAGGAGTGCCTCTGATGGGGCTG
 GCAATGACTGAGCAGGCGCCAGCCCGAGAGGACAGGAAGAGAGGACATATTGAGGAGGTGCAAGAGTGAAGCGCCG
 GTGTAGAAATGACTGCCCTGGAGGGTGGTTCTTGGCCCTGGCAGGGTGTGCTGACCTTACCTGTCAAAACACA
 AAGAGCAGGACTCCAGACTCTCTTGTGAATGGTCCCTGCGCTGCGAGCTCCACCAAGAGGCTTCTGCTGGCCCC
 ACTCTTGTAGCTTGGGTGGCTGGTGCACTGCCACTGTGCCGTGGTACCCCTGGCATGTTCCCTGCCCCCTCA
 GTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCGCTGCTCTACCGCGAGGCTACCACTGTGGACTGCAATGA
 CCTATTCTGACGGCAGTCCCCCGGCACTCCCGCAGGCACACAGACCTGCTCTCTGACAGACCAACAGCAATTGT
 CCGTGTGGACAGATGAGCTGGGCTCACTGGCCAAATCTCAGAGAGCTGGAACCTGTCCAGAAACAGCTTTTGGGA
 TGCCCGAGACTGTGATTTCACTGGCTGGCCAGCTGTGAGCTGCACCTAGAGGAGAACAGCTACCCGGCT
 GGAGGACCAACAGCTTTTGACGGGTGGCCAGCCTACAGGAACCTATCTCAACACCAACAGCTCTACCCGATCGC
 CCCCAGGGCTTTTCTGGCTCTGCAAACTTGTGCGGTGACCTCAACTCCAACTCTCTGAGGGCACTGCCAG
 CCGCTGGTTTGAATGTGCCCCAATCTGGAGATCACTATGATTGGCGGCAACAGGTAGATGCCATCTCTGGACAT
 GAACCTTCCGGCCCTTGCCCAACTGCTGAGCTTGGTGCTAGCAGGCATGAACCTGCGGGAGATCTCCGAGTATGC
 CTTGGAGGGCTGCAAGGCTGGAGAGCCTCTCTTCTATGACAAACAGCTGGCCCGGGTGGCCAGGCGGGCACT
 GGAACAGGTGCCCGGCTCAAGTGTCTAGACCTCAACAGAACCCGCTCCAGCGGTAGGGCGGGGACTTTTGC
 CAACTGCTGCACCTTAAAGAGCTGGGACTGAACAACTAGGAGGAGCTGGTCTCCATCGACAAGTTTGGCTGGT
 GAACTCCCGGCTGACCCAGCTGACATCAACAATAACCCACGGCTGCTCTTCCATCCACCCCGCCCTGCCA
 CCACTGCGCCAGATGAGAGCCTCATGCTCAACAAACACGCTCTCAGTGGCTTGCCACCGAGCGGTGGAGTC
 CTTGCCCACTGAGAGGCTGCTCCACGGCAACCCATCCGCTGTGACTGTGTCACTCCGCTGCGCCCAATGC
 CACGGGCAACCGGTGCGCTTCACTGAGCGCAATCAACCTGTGTGCGGAGCTCTCGGACCTCCAGCGCTCCC
 GGTGCGTGAAGTGCCCTTCCGGGAGATGACGGACCTGCTGCAATTTGGCCCTCATCTCCCAAGAGGCTTCCCCNAG
 CTTCCAGGTAGCCAGTGGAGAGAGCATGTGTGCTATGGCGGGCACTGGCCGAACCCGAACCCAGATCTACTG
 GGTCACTCCAGCTGGGCTTGCATGACACTTGCCTATGCAGGCGAGGAGTACCGGGTGTACCCCGAGGGACCT
 GGAGCTGCGGAGGGTGCAGGAGAGAGGCGAGGCTATACACTGTGTGCGCCAGAACCTGCTGGGGCTGACAC
 TAAAGACGTTAGTGTGTTTGTGGGCCGTGCTCTCTCCAGCCAGGCGAGGACAGGAGCAGGGGTGGAGCTCCG
 GGTGCAGGAGACCCACCCCTATCACATCTGCTACTTGGGTCAACCCACCAACACAGTGTCCACCAACTCAC
 CTGCTCAGTGCTCTCTCCCTCGGGGCGAGGGGCCACAGCTCTGGCCGCTGCTCTCGGGGAACCCACAGCTA
 CAACATTAAACCGCTCTCTCAGGCCACGGAGTACTGGGCTGCTGCAAGTGGCTTTGCTGATGCTCCACCACTCA
 GTTGGCTTGTGATGGGCCAGGACAAAGAGGCCACTTCTTGCCACAGAGCTCTTAGGGGATCGTCTGGGCTCAT
 TGCCATCTGCTGCTCTGCTCTCTCTCTGCGAGCTGGGCTAGCGGCCCACTTGGCAACGGCCAAACCCAGGAA
 GGGTGTGGGTGGGAGCGGCGCTCTCCCTCCAGCCTGGGCTTCTGGGGCTGGAGTGCCCTTCTGTCCGGGTGT
 GTCTGCTCCCTCGTCTGCTGCTGGAATCAGGGAGGAAGCTGCCAGATCTCAGAGGGGAGACACTGTTGCC
 ACCATTGTCTCAAAATTTCTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACATCTTTTACCAAA
 AGAGAAGAGCTTGGCCCACTGCTCCGCAAGAAAGGACATGGACCCAGCTCTTGAGGCTGGCAGCTGGGC
 CAAGCAGATGAGGGCTTTTGTGGCCCTGGGGGTGCTTCTGCAGCTTGAAAAAAGTTGCCCTTACCTCTCAGGGTCA
 CTTCTGCTGCCAATTTCTGAGGAACATCTCCAAGGAACAGGAGGGACTTGGCTAGAGCTCTGCTGCTCCCATCTT
 CTCTCTGCCAGAGGCTCTGTTGGCCTGGCTGGCTGTGCCCTCACTGTGTCCCGGGCTGCACCCCTCTCTCTTC
 TCTTTCTGTACAGTCTCAGTTGCTTGTCTTGTGCTCTGTCAGGCTGGAAGGGCTCAAGGAGGCTCATCATCAC
 TCGGGGGGCTGCCCTCAATGTGGAGGTGACCCAGCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAA
 CGCTCATCTCAGCAGCTGGCTGGGATTCGAAGCTGACTTTCTATAGCAATTTTGTAGCTTTGTGGAGAA
 ATGTGTCACTCCCCCAACCGATTCACTCTTTCTCTCTGTTTGTAAAAATAAAAAATAATAACAATAAA
 AAAA

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FIGURE 86

MRLLVAPLLLA WAGATATVPVVPWHVPCPPQACACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTL LLSQNSIVRVDPQSELGYLANLT ELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASIQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSILVLAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPG LKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNL P
ELTKLDITNNPRLSFIHPRAFHL PQMETLMLNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFI EPQSTLCAEPPDLQRLPVRVVPFREMTHCLPLISPRSFP PSLQ
VASGESMVLHCRALAEPEPIYVWTPAGLR LTPAHAGRRYRVYPEGTLELRRTAEAGLYT
CVAQNVLGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPHYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLLAAGLAAHLGTGQPRKGVGGRPLPPAWAFWGSAPSVRV V
SAPLVLPWNPRGKLRPSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

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FIGURE 87

GCAAGCCAAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT
 CTA~~ATG~~CGGCGAGACCATCATCAAGGTGATCAAGTTTCATCTCATCATCTGCTACACCGTCTACTAGTGSCACAA
 CATCAAGTTCGACGTGGAGCTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGGCTACCGTCTGTCGCCACCC
 CCTGGCCACACTCTTTCAGATCTCTGGCGTCTCTTACATCAGCCTAGTCACTCTTCTACCGGCCTCATCTGCATGTA
 CACACTGTGGTGGATGCTACCGCGCTCCCTCAAGAAGTACTCGTTTGAGTGCATCGCTGAGGAGAGCAGCTACAG
 CGCATCTCCCGACGTCAAGAAGCAGCTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCTCTACTCCAA
 GCGCTTCGCGCTCTTCCTCTCGGAGGTGAGTGAGAACAAAGCTGCGGACGCTGAACCTCAACAAACGAGTGGACGCT
 GGACAAGCTCTCGGAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACTCTGTTTCATGCTCAGTGGGATCT
 CCTGACACTGTGTTTGAACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCGCC
 CAGCATTTGCCAGCTCAGCGGCTCAAGGAGCTGTGGCTTACCAACACAGCGGCGCAAGATTGAAGCGCCTGGCGCT
 GGCTCTCTGCGCGAGAACCTGCGGCGCTGCACATCAAGTTCACGACATCAAGGAGATCCCGCTGTGGATCTA
 TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAAACCGCTACATCGTCATCGA
 CGGGCTCGGGGAGCTCAAAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCA
 AGATGTGGGCGTGACCTGCGAGAAGCTGCTCATCAACAATGAGGGCACCAAGCTCATCGTCTCAACAGCCTCAA
 GAAGATGGCGAACCTGACTGAGCTGGAGTGCATCGCTGCGACCTGGAGCGCATCCCCCACTCCATCTTCAGCCT
 CCACAACCTGCAGGAGATTGACCTCAAGGACAAACACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT
 GCACCGCTCACCTGCCTTAAAGCTGTGGTACAAACACATCGCCTACATCCCCATCCAGATCGGCAACCTCACAA
 CCTGGAGCGCCTCTACTGTAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTCTTCTATGCGCCAGCTCGC
 CTACCTTGGACCTCAGGCCACAACTGACCTGACCTTCTCCTCGCGCATCGGCTCTCTGAGAACCTCCAGAACCT
 AGCCCTCAGCGGCAACCGGATCGAGAGCTCCTCCGAGCTCTTCAGTGCAGGAAAGCTCGGGCGCCTGCACCT
 GCGCAACACCGTGTGCTGCTGACCTGCCCTCAGGGTGGCGAGCTGACCAACCTTGACGAGATCGACTCGCGGG
 CAACCGCTGGAGTGCCTGCTGTGGAGCTGGGCGAGTGGCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA
 GGACCTGTTCAACACATGCTCACCCGAGGTGAAGGAGCGGCTGTGAGAGGCTGACAAAGGCTGAGGCGAG
 GCGCGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGGAGGGCGAGGCTGACTTCTCCAG
 AACTCCCGGACAGCGCAGGACAGCCTCGCGGCTGGCGAGGCTCGGGGCGCTGTGTGATGCTGCGCCAGAGCGAGA
 GGACAGTATCTGTGGGCTGGCCCTTTCTCCCTCGAGACTCAGTGCCCCAGGGCAAGTGGTGTGGAGGAG
 AGCAAGTCTCAAGAGCGCAGGATTTGGATAATCAGGGTCTCCCTCGGAGGCGAGCTCTGCCCCAGGGGCTGAG
 CTGCCACAGAGGCTGGGGACCTCACTTTAGTCTTGGTATTTATTTTCTCCATCTCCGACCTGCTCATCC
 AGATAACTTATACATTTCCAAAGAAAGTTCAAGCCAGATGGAAGGTGTTTCAAGGAAAGGTGGGCTGCTTTTCCC
 TTGTCTTATTTAGCAGTGCCGCGGGCATTAAACACCCACCTGGAATTCAGCAGAGTGGTCCGGGCGAACCG
 CCATGGGACGCTCACCCAGCAGTGCCTGGGCTGGGCTCTGCGGTGCGGCTCCAGGGAGAGCAGGCTCCAGCTGGA
 AAGGCCAGGCTGGAGCTTGCTCTCTCAGTTTTTGTGGCAGTTTAGTTTTTGTGTTTTTTTTTTTTTAAATCAAA
 AAACAATTTTTTTTAAAAAAAGCTTTGAAAAATGGATGGTTTGGGTATTAAGAAAGAAAAAAACTTTAAAAAA
 AAAAGACATAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGTTGGCAGTTTCCCTTGAGCAACAGCAGCCAGCT
 TGAACCTGTGTTTCTTCTCCCTGGGCGCAGGTTGACGGGTGCTTTCGCGATCTGGTGTGACCTTGGTCCAGGAGTT
 CIATTTGTTCTCGGGGAGGAGTTTTTTTGTGTTTTTTTGGGTTTTTTTGGTGTGTTTCTTTCTCTCC
 ATGTGTCTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGAGGAG
 ACTCGGGTTGGCTAATCCCGGATGAACGGTGTCTCATTCGACCTCCCTCTCGTGCCTGCCTGCTCTCCA
 CGCACAGTGTAAAGAGCCAAAGAGGACACTTCGCCAGACTTTGTTTCCCAACCTCTGCGGATGGGTGTGT
 CCACTGCCACCGCTGGCTCCGCTTCATCAGCCCTGTGCGCACTCTGTCCTTCAAGAGAGCAGACATTA
 GAGGCTGGTGGGAATGGGAGGTGCGCCCTGGGAGGCGAGGCGTGGTTCAGGCGCGTCCGCTCTCGGCGC
 CTGGAGTGACACAGCGCAGCTGCGCACCTGGTGGCTGGAAGCCAACTGCTTTAGATCACTCGGCTCCCACTT
 AGAAGGCTCCCGCTTAGATCAATCAGCTGGAACCTAAGGACAGTTTAGAGTCTTGTCTTAATGATTATGT
 CCACTCGGTGCTCGCTGATTTGTTGTTTTCTGCGTGTGTCATTGGATATATCTCAGAAATATGCACTAG
 CCTCTGACCAACATGAAGCAAAAATCGGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAA
 ATCTATAACAGAAAAAATCAAA

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FIGURE 88

MRQTIKVIKFIILICYTVYYVHNKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLEHLFMLSIGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLWI
YSLKTLLEELHLTGNLSEAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLLELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFQ
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKLRLHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

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FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCCGTACTTGTCAATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCCTGAACGCAGGAGCTGTCAATTGACT
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCAGACAGTTCCATTCTACATTTTCTCAGAGTCCATGGAGGAAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT
TGCCTTGGGTGATTCTGGATCTCCCTGTTGATTGCTGCTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
GATCATGAAACAGAACACAGATGGGGTGAACCTCTATAACATCTTAACTAAAAGCACTCCCA
CGTCTACAATGGAGTCAGAGCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCAGCGC
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGCTTTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCTG
GGTGCGGAAACTGAAAGTGCCAGAAGTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGT
ACAGTGACCCATAAATCTTTGGAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCTTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTCAGCAAGAATAGCATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGCTCTCT
GGAGGCAATTTGGAATATTATTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

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Signal sequence:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCCTGGG
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATCACCCCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTCGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCCAAGGCGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACCTTTGAGTGGATCCAGAAG
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTTCTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGTGTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 92

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLRW
DSHVCVSVLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSN
YLSPRYLGNSPYDIALVKLSAPVTTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSSGGPLACNKG
LWYQIGVVSWSVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

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FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT
 CTTTGGCCCTCATCTCTCTGGCAAAATGCAGTTACAGCCCGGAGCCCGACAGCGGAGGACGC
 TGCCCCCAGGCTGGGTGTCCCTGGGCCGTGCGGACCCTGAGGAAGAGCTGAGTCTCACCTTT
 GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTCGGATCCAG
 CTCTCCTCAATACGGAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
 CACTGACCCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGAGGCCAGAAGTGCCATTCT
 GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
 TGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAACCCATGTTGTAAGGTCCCCAC
 ATCCCCTACCAGCTTCCACAGGCCCTTGGCCCCCCTATGTGGACTTTTGGGGGGACTGCACCGT
 TTTCCCCCAACATCATCCTGAGGCAACGTCCTGAGCCGCAAGTGACAGGGACTGTAGGCTC
 GCATCTGGGGGTAACCCCTCTGTGATCCGTAAGCGATACAACCTTGACCTCACAAAGACGTGG
 GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCTGGAGCAGTATTTCCATGAC
 TCAGACCTGGCTCAGTTCATGCGCTCTTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC
 CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCCGGGATGAGGCCAGTCTAGATGTGCAGT
 ACCTGATGAGTGCTGGTGCCAAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
 GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
 GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGTCA
 ACACTGAGCTCATGAAGCTGCCGCTCGGGGTCTCACCTGCTCTTCGCTCAGGTGACAGT
 GGGGCCGGGTGTTGGTCTGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG
 CCCCTATGTCAACACAGTGGGAGGCACATCCTTCCAGGAACCTTTCTCATCAAAATGAAA
 TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCACGGCCCTTCATACCAGGAG
 GAAGCTGTAAACGAAGTTCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC
 CAGTGGCCGTGCCTACCCAGATGTGGCTGCACTTTCTGATGGCTACTGGGTGGTCAGCAACA
 GAGTGGCCATTCATGGGTGTCCGGAACTCGGCCCTCTACTCAGTGTTTGGGGGGATCCTA
 TCCTTGATCAATGAGCACAGGATCCTTAGTGCCCGCCCCCTCTTGGCTTTCTCAACCCAG
 GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCTGTCT
 TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCTGGCTGGGATCCTGTAACAGGC
 TGGGGAACACCAACTTCCAGCTTTGCTGGAAGACTCTACTCAACCCCTGACCCCTTCTCTATC
 AGGAGAGATGGCTTGTCCTCCCTGCCCTGAAGCTGGCAGTTTCAGTCCCTTATTTCTGCCCTGTTG
 GAAGCCCTGCTGAACCTTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
 TGCTGTGAGCTTGACTTGACTCCCAACCTACCATGCTCCATCATACTCAGGCTTCCCTACT
 CCTGCTTAGATTCTCTAATAAGATGCTGTAACCTAGCATTTTGAATGCGCTCTCCCTCCGC
 ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTGTATACAGACTCTGTGCACTA
 TTTCACTTGATATTCAATCCCCAATTCAGTGCAAGGAGACCTCTACTGTACCCGTTTACTCT
 TTTCACTCCCTGACATCCAGAACAATGGCTCCAGTGACATCTTCTCAATCTTTGCTTTATG
 GCCTTTCCATCATAGTTGCCCACTCCCTCTCTTACTTACTAGCTTCCAGGTCTTAACCTTCTGT
 ACTACTCTTGTCTTCTCTCTCATCAATTTCTGCTTCTTCATGGAAATGCTGACCTTCAITGC
 TCCATTTGTAGATTTTGTCTTCTCAGTTTACTACTGCTTCCCTGGAAACAAATCACTGACA
 TCTACAAACCATTACCATCTCACTAATAAGACTTCTATCCAAATAATGATTGATACCTCAAA
 TGTAAAAA

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FIGURE 94

MGLQACLLGLFALILSGKCSYSPEDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLLENVADLVRPSPLTLHTVQKWLALAAGAKCHSVITQDFLTCWL
SIRQAELLPLGAEPHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMASAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDDESLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVIPWVSGTSASTPVFGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

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FIGURE 95

GCCGCGCGCTCTCTCCCGCGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGC
GGGCTGCTCGGCGCGGAACAGTGTCTCGGCATGCGAGGGATTCCAGGGCTCCTCTTCTTCTC
TTCTTTCTGCTCTGTGCTGTTGGGCAAGTGAGCCCTTACAGTCCCCCTGGAAACCACTTG
GCTGCATACCGCTCCCTGTGCTTGTGCCCCAGTCTACCTCAATTTAGCCAAGCCAGACT
TTGGAGCCGAAAGCCAAATTAGAAGTATCTTCTTCAATGTGGACCCAGTGTCTAAGGGAAC
CCTGTCGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCCAATGG
CAGCCGCACAGAGACGCAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGC
AGGTTCAGCATTTTTGGGAAGGACTTCCTGCTCAACTACCCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCTGGTGGCAGAGAAGCATGTCTCAGCTGCCCACTGCA
TACAGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCCTAAAGCCC
AAGTTTAAAGATGGTGGTTCGAGGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA
ATTTCACTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCTCAAAAAGCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGCAGAAATCACTTCTC
TGGTTATGACAATGACCGACCAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGTCTTACCAGCAATGCGATGCCAGCCAGGGGCCAGCGGGTCTGGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTTTCAGG
GCACCACTGGGTGGACATGAATGGTTCCCCACAGGATTTCAACGTGGCTGTGAGAATCACTC
CTCTCAAATATGCCAGATTTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGTTCCCTCCTGGCAGCAATTAAGGGTCTTCATGTTCTTATTTTAGGAGAGGCC
AAATTGTTTTTTGTCTATGGCGTGCAACGTGTGTGTGTGTGTGTGTGTGTGAAGGTG
CTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACTATTTGAAAAC
GTTTGTGTATCATATCATATATCATTTAAGCAGTTTGAAGGCATACTTTTGCATAGAAATAA
AAAAAATACTGATTTGGGGCAATGAGGAATATTGACAATTAGGTTAATCTTCAGTTTTTG
CAAACCTTGATTTTTATTTCATCTGAACCTGTTTCAAAGATTATATTAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

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FIGURE 96

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAAYRLPVVLPQSTLNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKS
RRKRQIYGYSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD
AQPASGSGVYVRMWKRQQKWERKIIIGIFSGHQVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

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106170.2254060

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCCTGCCTGCTCCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCTCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCCTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCCACTGTTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCTGTGTATTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCTCAGACCCCTGCAGAAGCTGAAGGTTCCCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGAGCGCAACAGGCCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCCCGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCCCAACGGCCTCATGTCCCCGCCCCAC
GACTTCCGGCCCCCCCCGGCCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTAT
AGGTATTGTAAACCTGCCACATATCTTATTTATTCCTCCAATTTCAATAAATATTATTAT
CTCAAAAAAAAAA

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FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAAARIPVPPACGKPKQLNRVVGEDSTDSEWP
WIVSIQKNGTHHCAGSLTSLRWVITAACHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIISWEGECAERNRPGVYISLSAHRSSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCTGATGCTTCTGCTGCCGCTACTGCTA
 CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGTGGT
 GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
 GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCCTACGCACGGCAGTGCCTGTGGGGCCAC
 AACAAAGAGCGCGGGCGCCGCGGCGAGAATCTGTTTCGCCATCACAGACGAGGGCATGGACGT
 GCCGCTGGCCATGGAGGAGTGGACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
 GCAGCCCAAGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
 GGTGTGGTTCCTCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
 GGTGTGCAACTATGAGCCTCCGGGGAACTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
 CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
 CCGGAAGATGCTCAGGATTTCCTTACCTGGTAAGTGAAGGCCCATCTTCCGGGCGACTGA
 AGCATCAGACTCTAGGAAAAATGGGTACTCTTCTTCCCTAGCAACGGGGAITCCGGCTTTCT
 TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCATGGCC
 CCAACTTCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC
 AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA
 CCTTCCCCAAATCGACCCATGTTCTATCCCCAAATCAGCAGACAAAGTGACAGACAAAACA
 AAAGTGCCCTCTAGGAGCCAGAGAACTCTTGAGCCCAAGATGTCCCTGACAGGGGCAAG
 GGAACCTCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCTTCCAGTG
 AGGTCTTGCCCTCAGTTTTCAGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
 CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTTCCCCAATACCTCTGCCACCGCTAA
 TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA
 AGCCTAGCGTGTGTGCAGGGCTGAACTCGGGCCCTGGTTCATGTGTGGGGCCCTCTCCTGGGA
 CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACCTCAAAGGG
 TGAAGAGGTGAGCTGTCTCCTGTGCATCTTCCCCACCCTGTCCCAGGCCCTAAACAAGATA
 CTTCTTGGTTAAGGCCCTCCGGAAAGGGAAAGGCTACGGGGCATGTGCCCTCATCACACCATCC
 ATCCTGGAGGCACAAGGCCCTGGCTGGCTGCGAGCTCAGGAGCCGCGCTGAGGACTGCACACC
 GGGCCACACCTCTCCTGCCCTCCTCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCT
 CACTGCCTACCTGGCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCTGAGTGCTCTG
 TGTAGCTGGGGATGGGATTCCTAGGGGAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
 TTTGAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACCTCTGACTCTCCAATAAAAACTT
 GTCCAACCTGTGAAA

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FIGURE 100

MHGSCSFLMLLLPLLLLLLVATTGFPVGALTDEEKRLMVELHNLVRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCQVWGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLFYLVTAPSFRAATEASDSRKMGTSSSLATGIPAFVLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPVTTTEVPSSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENS LDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSSLPGAEGPDKPSV
SGLNSGPGHVWGPLLGLLLLPLVLGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAAC TGAAGTCAGGCTTTTCATTTGGGAAGCCCCCTCAACAGAAATCGGTCATTCTCCAAGTTATGGTGGACGT
 ACTTCTGTGTCTCCCTCTGCTGCTTTTTCACATTAGCAGACCGGACTTAAGTCACACAGATTATCTTTCAT
 CAAAGGCAAGTTCCATGAGCCACCTTCAAAGCCTTCGAGAACTGAAACTGAACAACATGAATGGAGACCATTC
 AAATCTGGGACAGCTCTCGGCAAAATATTACACTTCTCTCCCTGGCTGGAAACAGGATTTGTGAAATACCTCCCTGA
 ACATCTGAAGAGATTGAGTCCCTTTGAAACCTTTGGACCTTAGCAGCAACAATATTTAGAGCTCCAAATGTCATT
 TCCAGCCCTACAGCTCAAAATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACTCGGGATTTTGAACA
 TTTGGCCAAACCACTCTCTGTGTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCAACCAGATGTTTAAACT
 GCCCCAACTGCAACATCTCGAATGAAACCGAAACAGATTAATAATGTAGATGGAGCTGACATTCGAAGCCCTGG
 TGCTCTGAAGTCTCTGAAATCTGAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGGCTGAGCAA
 CATGGAAATTTTTCAGCTGGACCAATAACAACCTTAACAGAGATTAACAAAGGCTGGCTTTACGGCTTGTCTGATGCT
 GCAGGAATCTCATCTCAGCCAAAATGGCCATCAACAGGATCAGCCCTGATGCTGGAGATTTTGGGGGCTGAGCA
 TGAGCTGGACCTTAACCTTCAATCACTTACAGGTTAGATGATTCAAGCTTCTTGGCCCTTAAGCTTACTAAATAC
 ACTGCACATTTGGGAACACAGAGTCAGCTACATTTGCTGATTGTGCTTCCGGGGCTTTCCAGTTTAAAGACTTT
 GGAATCTGAAGAACAATGAAATTTCTGGACATTTGAAGACATGAATGGTCTTTCTTGGGCTTGACAACTGAG
 GCGACTGATATCTCAAGGAAATCGGATCGTCTTATTTACTAAAAAAGCCTTCACTGGTTTGGATGCATTTGGAGCA
 TCTAGACCTGAGTGACAAACGCAATCATGCTTTTACAAGGCAATGCAATTTTACAATAAGAAACCTGCAACAAT
 GCATTTAAATACATCAAGCTTTTGTGCGATTTGCCAGCTCAAAATGGCTCCCAAGTGGGTGGCGGAAACCACTT
 TCAGAGCTTGTAAATGCGAATTTGTGGCCATCTCAGCTGCTAAAGGAAAGAACATTTTGGCTGTAGCCGAGA
 TGGCTTTGTGTGTGATGTTTCCAAACCCAGATCAGGTTCCAGCAGAAACACAGTGGCCTCAATAAGGTTT
 CAAATTTGAGTTTCACTGCTCAGCTGGCCAGCAGCTGATTTCCCAATGATCTTTGCTGGAAAGAACAGATGA
 ACTACTCATGATGCTGAAATGAAAAATATGTCAGTGGGGGCAACCCAGCTGGAGGATGATGAGATATACCA
 CATCTCTCGGCTGGCGAGGTTGAAATTTGCGAGTGGGGGCAACCCAGCTGGAGGATGATGAGATATACCA
 ATCTACTCTCTGTCAGGCAAGCTTACAGTAAATATGCTTCCCTCATTTACCAAGACCCCATGATCTCACAT
 CCGAGCTGGGGCAATGGCAGCTCTGGAGTGTGCTGCTGGGGGCAACCCAGCTGGAGGATGATGAGATATACCA
 TGGGGGCAAGACTTCCAGCTGCGAGGAGAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 GAT
 AACTCTGACTGCTTAGAAACACCATCATTTTGGCGGCACTGTTGGAGCGCAATGTAACCAAGGCGAAGAACG
 CGTCTCAAGTGCATCTGGAGGAAAGCCCTCCCTTAACTGAACCTGGAACCAAGATGATGAGCTTGTGTGT
 AACCGAGAGGCACTTTTTCAGCAGGCAATCAGCTTCTGATTTATGTTGGAGCTCAGATGTCAGTGTGCTGGGAA
 ATACACATGTGAGATGCTCAACCCCTTGGCACTGAGAGAGGAAACGTCGCTCAGTGTGATGCCACTCCAA
 CTGCGACTCCCTCAGATGACAGCCCATCGTTAGACGATGACGGATGGGCACTGTTGGGTGTGCTGATCATAGC
 CGTGGTTGCTGTGTTGGGGCACTGCTGCTGTTGGGTGCTCATATATACCAACAAGGCGAGGAATGAAGA
 TTGAGCATTACCAACACAGATGAGACCACTTGGCAGCAGATATCTTAGTTATTTGTCATCTCAGGGAACGTT
 AGCTGACAGGCGAGGATGGGTACGTGCTTTCAGAAAGTGAAGCCACCACTTTTGTCACTCTTCAGGTGCTGG
 ATTTTCTTACCAACAACATGACAGTAGTGGGACCTGCCATATTGACAAATAGCAGTGAAGCTGATGTGGAGCTGC
 CACAGATCTGTTCTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTGAAAGGAAATGTGATGGCTCAGA
 TCCCTTTGAAACATATCATACAGGTTGCACTGCTGACCAAGAACAGTTTAAATGGACCACTATGAGCCAGTTA
 CATAAAGAAAAAGGATGCTACCCATGTTCTCATCTTCAGAAATCTGCGAACCGAGCTTTCAGTAAATATTA
 GTGGCCTTTCATGTTGAGGAGCTACTTAAACATAGTTACTCTCACAATGAAGGACCTGGAAATGAAAAATCTGT
 TCTAAACAAGTCTCTTTCAGTTTTCAGTTTTCAGGAGCCAGCTGCTGCTGAGTAACTTTTCATGGG
 TACCCTTTGAAAGCTCTCAGGAGACCTCACCTAGATGCTTATCAAGCTTTGGACAGCCATCAGATTGTGACGCC
 AAGAGCTCTTTATTTGAAAGCTCATTTCTCCAGACTTGGACTCTGGAGGAAAGATGGGAAAGAAAGGAC
 AGATTTTTCAGGAGAAATACATTTGTACCTTTAAACAGACTTGAAGAACTACAGGATCTCMAATTTTCAGTCT
 TTATGACTTGGACATAGACTGAAATGAGACCAAGGAAAGCTTAAACATACACTCACTCAAGTGAACCTTTTAACT
 AAAAGAGAGAAATCTTTATGTTTTTAAATGGAGTTATGAAATTTTAAAGGATAAAAATGCTTTATTTACAGAT
 GAAACAAAATTTACAAAGTTATGAAATTTTATATCTGGGAATGATGCTCATATAAGAAATACCTTTTAAACTA
 TTTTAACTTTGTTTTTTCAGCAAAAGATCTTACGTAATTAATGATATAAATCATGATGATTTTATGATTT
 TTATATGCGAGATTTCTTTTATGAAAAATGAGTTACTTAAAGCATTTTAAATATACCTGCTTGTACCATTTT
 TTAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAA

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FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLNLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNIRISAI PPKMFKLPLQLHLELNRRNIKNVDGLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMEILQLDHNNTLBITKGWLYGLMLQELHLSQNAINRISPDWE
FCQKLSLELDLTFNHLRLDDSSFLGLSLNLTNLHIGNNRVSYIADCAFRGLSSSLKTLDLKNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSI TTKAFTGLDALEHLDSLDAIMSLQGNAFSQ
MKKLQQLHLNLTSSLLCDCQLKWLPLQWVAENNFQSFVNASCAPHQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAHLEAQQ
GEVMEYTTILRLREVEFASEGKYQCVISNHFSSSYSVKAKLTVNMLPSFTTKTMDLTIRAGA
MARLECAAVGHPAPQIAWQKDGDTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLITVLETPSFLRPLLDRTVTKGETAFLQCIAGGSPPPKLNWTKDDSPLVVTER
HFFAAGNQLLIIVSDSDVADAGKYTCESMNTLGTGRGNVRLSVIPTPTCDSPQMTAPSLDDDG
WATVGVVIIAIVCCVVGTSVLVWVVIYHTRRRNEDCSITNTDETNLPAIPSYLSSQGTILAD
RQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDFPFTYHTGCSPPDRPTVLMDDHYEPSYIKKCEYPCSHPSEESCSERSFSNLSW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSNPEPASVASSNSFMGTGFKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLNRYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGSAGACTTTTTTTTTTGGTGGTGGTGGCTGGTGGCTGCGCTGCAAAAAATG
AAGGATGCGAGGCGCGAGCTTTCTCTGGAAACCGAACCGCAATGGATAAATGATTTGTCGAAGAGAGAAGGAGAAC
GAAGCTTTTTCTTTGGAGCCCTGGATCTTAACACAAATGTGTATGTGTGCACACAGGAGCATTCAAGAATGAAA
TAAACACAGAGTTAGACCCGCGGGGGTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCTCC
CACCCCCAAAAAAGGATGATTGGAAATGAAGAACCAGGAGTTCAAAAAGAAAAAGTATGTTCATTTTTCTC
TATAAAGAGAGAAGTGAAGCCAGGAGATATTTTGGAAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAAAGAACT
GGTGTGGTGGTGTCTTTCTTTCTTTTGAATTTCCACAAGAGGAGAGAAATTAATAATACATCTGCAAAAGAAA
TTTCAGAGAAAGAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACAGCAGAGCAGATTGGA
TTTGTGCTTATGTTGACTAAAAATGACGGATAATTGCAAGTTGGATTTTCTTCATCAACCTCCTTTTTTAAAT
TTTTATTCCTTTTGGATACAGATCATGCGTTTTCTCTGTTCTTAAACACCTGGATTTCATCTGGATGTGCT
GTGATCAGTCTGAATACAACTGTTTGAATTCGAAGGACCAACACAGATAAATTATGAATGTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAAACAGGGCCCTATTGACCCCTGCTTGGTGTCT
GCTGGCTCTTCAACTTCTTGTGGTGGTGGTCTGGTGGCGGCTCAGACCTGCCCTCTGTGTGCTCCTGCAGCAA
CCAGTTGACAGAGGTGATTGTGTTCCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCT
GCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATGGGGCTTCAATGGTCTGGCGAACCTCAACACTCTGGA
ACTCTTTGACAACTCGTCTTACTACCATCCGAATGGAGCTTTGTATCTTGTCTAAACTGAGGAGCTCTGGTT
GCGAAACCAACCCATTGAAAGCATCCCTTCTTATGCTTTTAAACAGATTCTCTTTGCGCGAGCTAGACTTAGG
GGAATTGAAAAGACTTTCAATCATCTCAGAAGGTGCTTTGAAGGTTCTGCCAATTGAGGTATTTGAACCTTGC
CATGTGCAACCTTCGGGAACTCCCTAACCTCACAACGCTCATAAACACTAGATGAGCTGGATCTTTCTGGGAATCA
TTATCTCTGCGATCAGCTGGCTCTTTCCAGGGTTTGTGACCTCTCAAAAACCTGGGATGATACAGTCCAGAT
TCAAGTGAATTGAACGGAATGCTCTTTGACACCTTCACTGCTAGTGGAGATCAACCTGGCACAACATAATTAAC
ATTACTGCTCATGACCTTCCTCACTCTGCACTCTAGAGCGGATACATTTAATCAACACCTTGAAGCTG
TAACACTCTCTCAACTTAAAGGGAGGTACATTTGAGAGCTCGACAGAAATTAATCACTGATTAAGTCTCGGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAGAGCATGCGAGCTGAGCTGAAATGTGGGCCCTCAACATC
CCTGACATCTGTATCTTGGATTACTCCAAATGGAAAGTCAATGACATGAGGCGGTACAAAGTGCAGTAGCTGT
GCTCAGTGATGTTAGTTAAATTTACAAATGTAACTGTGCAAGATACAGGCATGTACATGATGTGTGAGTAA
TTCCGTTGGGAATACTACTGCTTCAGCCACCTGATGTTACTGAGCAACCACTACTCTTTCTTACTTTTT
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCAAGGACCAAGATAACATGATGGGTCCCACTCC
AGTGGTGCAGTGGGAGACCAATGTGACCACTCTCTCAACCCACAGAGCACAAGGTGCAGAGAGAAACCTT
CACCATCCCAGTGACTGATATAAACAGTGGGATCCAGGAATTTGATGAGGTGATGAAGACTACCAAAATCATCAT
TGGGTGTTTTTGGGCCATCACTCATGGCTGCAGTGATGTGTGTCATTTCTACAAGATGAGGAAGCAGACCA
TCGGCAAAACCATCACGCCCAACAGGAGCTGTTGAAATTTAATGATGGATGATGAGATTACGGGAGACACAC
CATGGAAGCCACCTGCCCATGCTGCTATCGAGCATGAGCACTAAATCATATAACTCATACAAATCTCCCTT
CAACCACACAACACAGTTTAAACAAATAAATTAATAACAGATTGAGTGCATGAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAACTTAAACAATTACAGAGTTTACAAAAACAAACAAATCAAAAAA
GACAGTTTATTAATAATGACACAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAA
AAAAGAAAAGAAATTTATTATTAATAATCTATTGTGATTAAGCAGACAAAA

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FIGURE 104

MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGI STNTRLLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHHPWNCNCDIL
WLSWWIKDMAFSNTACCARCNTPPNKGRIYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIVLSDGTNLNFTNTVTQDTGMYTCMVNSVGN
TTASATLNVTAATTPFSYFSTVTVTETMEPSQDEARTTDNNVGPTPVVDWETTNTTSLTPQ
STRSTKFTFTIPVTDINSIGIDVEMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEBITGDTPMESHLPMPAIEHEHLNHVNSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCCTTCGGTTTCCCTCTGCTGTTTGGGGGCA
TGAAGGCGCTTCGCGCGCGGAGTTAAAGAAGGAATTGACCGGCGAGCGCGAGGAGGAGCGCGCAACGCCACCGC
GAGGCGCGGCGTGCAACCTCGGCTGGGAAGTTTGTGCGCGGCGCGGAGCGCGCGCTGGGAGCTTCGGGTAGAG
GACCTTAGGCGCGTGCGACCGCGCTAGGAGCGCGCGGAGCTTCGGTGCGCGCGCGCGGGGTGGGGCTGCTGTGTGC
GCGGTGTTGGGGCGCGCTGCGCGCTCCGACAGCGCGCGGTGCGCGGGAATCTCGGGGAGCCCTCTGGGTGAGTCCGCT
GAGCGGCCATGCCCCACTACCTGCGCGCTGCTCGGGGACCTGCTGGAGCTGCAGTCTGTAAGCGCGCTAGCGCGCTTCT
CCGAGGCCATCTCCGCTCTGGGTGCTGCTCGGCTGGACTTAAAGTCAACAAGATATATCTTTCATCAAGGCAAGTTCC
ATGAGCGACCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACAATGAATTTGAGAGCACTTCAAATCTGGGACCA
GTCTCGGCAAAATTTACACTTCTCTCTTGGCTGGAAACAGGATTTGTAATACTCCCTGAAACATCTGAAAGAG
TTTCAGTCCCTTGAACCTTTGGACCTTAGCAGCAACAATATTTAGAGCTTCAAACCTGCATTTCCAGCGCTTACAG
CTCAAAATATCTGTATCTCAACAGCAACCGAGTCACTCAATGGAACCTGGGTATTTTGACAATTTGGGCAACACA
CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCAACCAAGATGTTTAAACTGCCCACTGCAAC
CATCTCGAATTTGAACCGAAACAGGATTAATAATGTAGATGGACTGACATTCGAAGCCTTGGTGCTCTGAAGTCT
CTGAAAATGCAAGAAATGGAGTAAAGAACTTATGGATGGAGCTTTTGGGGCTGAGCAACATGGAATTTTG
CAGCTGGACCATAAACAACCTAACAGAGATTACCAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTCAT
CTCAGGCAAAATGCCATCAACAGGATCAGCCCTGATGCTGGGAGTTCTGCCAAGCTCAGTGAGCTGCACACCTA
ACTTTCACTCACTTATCAAGGTTAGATGATTAAGCTTCCCTGGCCTAAAGCTTACTAAATACACTGCAGATGGG
AACAACAGAGTGCAGTCACTTGTCTGATTTGCTCTCGGGGCTTCCAGTTTAAAGACTTTGGATCTGAAGAAC
AATGAATTTCTGCACTATTGGAAGCAATGAATGGTCTTTCTCTGGGCTTGACAACTGAGGCGACTGATATCTC
CAAGGAATCGGATCGGTTCTATTTACTAAAAAAGCTTCACTGGTTTGGATGCAATGGAGCACTAGACCTGAGT
GACAAAGCAATCTCTTTTACAGCAATGCAATTTTCAAAATGAAGAACTGCAACAATTTGCAATTTAAATACA
TCAAGCCTTTTGTGCGAATGTCAGCTTAAATGGCTCCCAAGTGGGTGGCGGAAACAACCTTTAGAGCTTTGTA
AATGCGAGTTGTGCGCACTCTCAGCTGCTAAAGGAAGAAGCAATTTTGTCTGTAGCCAGATGGCTTTGTGTGT
GATGATTTTCCCAACCCAGAGTCAAGGTTGAGCAGAAACACAGTCCGCAATAAAGGTTCCAAATTTGAGTTTC
ATCTGCTCAGCTCGCAGCAGCAGTGAATCCCAATGAATTTTGTCTGGAAAGAACAATGAACACTGCTCATGAT
GCTGAATGGAATAATGACACCTCCGCGCCCAAGGTGGCAGGTGATGGAATATACCACCATCTCTCGGCTG
CGCAGGTGGAATTTGGCAGCTGAGGGGAAATATCAGTGTGTCATCTCCCACTCTTGGTGTCACTCTACTCTGTC
AAAGCCAAAGCTTACAGTAAATATGCTTCCCTCATTCAACCAAGACCCCAATGAATCTCCATCCAGAGTGGGGCC
ATGCGCAGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCAGATAGCTTGGCAGAGGATGGGGCGCAGAC
TTCCAGCTGCAAGGGAGAGACGCACTGATGTGATGCGCGGAGGATGACGTGTTCTTATCGTGGATGGAAGATA
GAGGACATTTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTCAAGAAATGCAACTCTGACTGTCT
CTAGAAAACCACTCATTTTTGGCGGCACGTGTTGGACCGAACTGAACCAAGGGAGAAACAGCGCTCTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCATAACTGAACCTGGACCAAGATGATAGCCCATTTGGTGGTAACCGAGAGGCAC
TTTTTTGCAAGCAAGCAATCAGCTTCTGATTATTTGTGGACTCAGATGTCAGTGAATCTGGGGAATACACATGTGAG
ATGCTTAACACCTTTGGCAGCTGAGAGAGGAACAGTGCAGCTCAGTGTGATCCCACTCAACCTGCAGCTCCCC
CAGATGACAGCCCATCGTTAGACGATGACGGAATGGGCCACTGTGGGTGTGCTGATCATAGCCGTGTTGTGT
GTGGTGGGCAGCTCAGCTGTTGGGTGTTGTCATCATACCAAGCGGAGGAATGAAGATGTCAGCATATACC
AACAAGATGAGACCACTTGCAGCAGATATCTAGTTATTTGTCATCTCAGGGAACGTGAGCTGCAGCGCAG
GATGGGTACGTGCTTCAGAAAGTGGAGGCCACCAAGCTTTGTCACTCTTCAGGTGCTGGATTTTCTTACCA
CAACATGACAGTAGTGGGACCTGCCATATTGACAAATGACAGTGAAGCTGATGGAAGTGGCCACAGATCTGTTCT
CTTTGTCGGTTTGTGGGATCCAGCGCCCTATGTATTTGAAGGAAATGTGTATGGCTCAGATGCTCTTTGAAACA
TATCATACAGCTTGTGAGTCTGTGACCAAGAACAGCTTTAATGGACCACTTGAAGCAGATGTCAGCCAGAGGCTTTAT
GAGTGTCTACCATGTTCTTCACTCTCTCAGAAAGATCTCTGCGAAGCGAGCTTCAGTAATATATCTGTCGCTTCAAT
GTGAGGAAGCTCTTAACTACATAGTTACTCTCACAATGAAGGACTTGAATGAATAATCTGTGCTCTTAAACAGTTC
TCTTTAGATTTTATGTGCAAAATCAGAGCGCAGCGTCGGTGTGCTCGAGTAATCTTTTATGGGTACCTTTGAAAA
GCTCTCAGGAGCCTCAGCTAGATGCTTATTAAGCTTTTGGACAGCAGCTCAGATGTCAGCCAGAGGCTTTTAT
TGAAGCTCATTTCTCCCCAGACTTGGACTTGGGTGAGGAGAGATGGAAGAAAGAGACAGATTTTCAGGAA
ACATAGATCACATTTTACTTTTAAACAGACTTTAGAAAACTACAGACTCCTTAACTCTTTATGACTTGGAC
ACATAGCTGAATGAGACCAAGGAAAGCTTAACTACTACTCTCAAGTGAACCTTTTAAAGAGAGAGAGAT
CTTAGTGTTTTAAATGGAGTTATGAATTTTAAAGAGTAAATGCTTTTATTAACAGATGAACCAAAATATAC
AAAAAGTTATGAAATTTTATACCTGGGAATGATGCTCATATAAGAAATACCTTTTAACTATTTTAACTTTG
TTTTATGTAAGAAAGTATCTACGTAAATTAATGATATAAATCATGATTTTATGTATTTTATATATGCGACA
TTTCTTTTATGGAATAGTGTACTTAAAGCATTTTAAATATACCTGCTGTATCCATTTTAAATAGAGGTT
ACTTCATTATTTGCACTATATTTTAAATAAATGTGTCATTTGAAAAAAGAAAAAAAAAAAAAAAAAAAA

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FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLDDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDDLSSNNISELQTAFPAALQKLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNISAIPPKMFKLPLQLHLELNRNKIKNVDDLGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMBEILQLDHNNLTETKGLWLYGLLMLQELHLSQNAINRISPDWFC
QKLSELDLTFNHLRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSSLKTLDDLKNNIEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRISITTKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNTSSLLCDCQLKWLQWVAENNFQSFVNASCAPQLLKGRSIFAVSPDGFVCDFF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAQGGGE
VMEYTTILRLREVEFASSEGKYQCVISNHFSSSYSVKAKLTVMNMLPSFTKTPMDLTIIRAGAMA
RLECAAVGHGPAQIAWQKDGDTDFPAARERRMHVMPEDDVFFIYVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPELLDRITVTKGETAVLQCIAGGSPPPKLNWTKDSSPLVVTERHF
FAAGNQLLIIVDSVDSDAGKYTCMSNTLGTGERGNVRLSVIPTPTCDSPQMTAPSLDDDDGWA
TVGVVIAVVCVVGTSVLVWVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTLLADRW
DGVVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSSEADVEAATDLFLCPFLGSTGPMY
LKNVYGSDDPFETYHTGCSFDPRTVLMDHYEPSYIKKKECYPCHSPSEESCERSFSNLSWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTGFKALRRPHLDAYS
SFGQPSDCQPRAFYLLKAHSSPDLDSSGEEDGKERTDFQEENHICTFKQTLNRYTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

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FIGURE 109

GGGAGGGGGCTCCGGGCGCGCGCAGCAGACCTGCTCCGCGCGCGCGCTCGCGCTGCTCTCCGGGAGCGGCAG
CAGTAGCCCGGGCGCGAGGGCTTGGGGGTTCCTCAGACTCTCAGAGGGCGGCTCCCATCGGCGGCCACCACC
CAACCTGTCTCCGCGCGCCACTGCGCTGCGCGCCAGGACCGCGTGCCTCAACATGGATTTCCTCTGGCGCTGGT
GCTGGATCTCTCGCTTACTCTGCGGCGCGCGCCGAGTTTCAGACGGGAGGTGGCCAGGCAAAATAGTGTATCATGAT
TGGCCTATGTGCTTATGGTGGGAGGATGACTGCTGCTGGGGCTGGGCTCGCAGTCTTGGGACAGTGTCAAGC
TGTGTGCGCAACACGATGCAAAATGCTGGAATGTATCGGGGCAAAACAGTGCAGGTGTATCTGGTTATGCTGG
AAAAACCTGTAAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGGCTGTAAAGCAGAGTGCATGAACACTTA
CGGCAGCTCAAAATGCTACTGTCTCAACGGATATATGCTCATGCGGGATGGTTCCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACTGTCAAGTATGGCTGTGATGTTGTTAAAGGACAAATACGCTGCCAGTGCCTATCCCTGGCCT
GCACCTGGCTGCTGATGGGAGGACTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCTGGCCTAGATT
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCTAAAGGCTCGATCTCATGTATATTGGAGG
CAAAATATCAATGTATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTGTCTGATGTTATATA
CGTACGTGGGTCTTCAAGTGCAAAATGTAAGAAGGATACAGGGTGTGGACTGACTTGTGTATATATCCAAA
AGTTATGATTGAACCTTCAGGTCCAATTCAATGTACCAAAGGAAATGGTACCATTTTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTCTGATGTTGGAAGTACTTGGTGGCTCCGAAGACACCATATATTCTCTATCATTAACAA
CAGGCTTACTTCAAGCAACCAACAGACCTACACCAAAGCAACACCAATTCCTACTCTCACCACCACCAACC
CCTGCAACAGAGCTCAGAACACCTTACACCTACAAACCCAGAAAGGCCAACACCGGACTGCAACTATAGC
ACGAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAAACAGGGTACAGACAGCCCTCAGAAACCCAGAGG
AGATGTGTTTCAAGTGTCTGTGACACAGTTGTAATTTTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCATCGGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAAGCCCCAGG
GGGAAAAGCTGCACGCTTGTGCTACCTCTCGGCCGCTCATGCAATTCAGGGGACCTGCTGCTGTCAATCAGGCA
CAAGGTGACCGGGTGCACCTCTGGGACACTCCAGGTGTTTGTGAGAAAACCGGTGCCACGCGAGCAGCCCTGTG
GGGAAAGAGGTTGGCCATGGCTGGGAGCAAAACACAGATCACTTTCGAGGGGCTGACATCAAGAGCGAATCA
AAGATGATTAAGGGTTGCAAAAAAGATCTATGATGCAAAATTAAGAAATCGGGATATTGAGCCTGGAGAG
AGAAGATCAGGCGCAACCAATGATGTTTCAAGTATATGAAGGTTGCAACAGAGAGGTGGCGACAGCTG
TTCCTCATATGCACTAAGAAATGAACCAAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTTCCTGCGAGG
GGCCATTGTTAGAAATCTTCATAAAAAAGAAAGTGTGAAATCTCAGTATCTCTCTCTTTCTAAAAAATTAGA
TAAAAAATTGCTATTAAAGATGGTTAAAGATGTTCTTACCAAGGAAAGTAAACAATATAGAAATTTCCCAA
AGATGTTTGTATCTCTAGTAGTATGCAAGTAAAAATCTTTAGAACTAAATAAATTTGGACAGGCTTAATTTAGG
CATTTCCCTCTTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAGAGCCACCAAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTGGCAATCTAGCAGTATTAAAGAAAAAGGAAACTATTTATTCCAAATGAGAGTATGATGAC
AGATATTTTAGTATCTCAGTAATGTCTAGTGTGGGGTGGTTTTCAATGTTTCTCATGTGAAAGGTATAAGCC
TTTCATTTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTTTAAAGAGATCCTTCAAGGAAACAGGTTCAAGAG
ATTTTCATCGGGTGCAATCTCTCTGCTTCGTGTGTGACAAGTATCTTGGCTGCTGAGAAAAGAGTGCCCTGCC
ACACCGGAGACCTTCTCTTCACTCATCAGTATGATTCACTTCTCTTATCAATGGACTCTCCAGGTTTCCAC
AGAACAGTAATATTTTTTGAACAATAGGTACAATAGAAGGTTCTTGTGATTAACTGGTAAAGGCGAGGCTGG
AGGGGAAAAATAAATCATTAAGCCTTTGAGTAACGCGAGAATATATGGCTGTAGATCCATTTTAAATGGTTCAAT
TCTTTATGTGATATAACTGACAGAGAAATATCAAAAGTACTGTATAAATCACTTGTATTATTTAAATGTTT
CTAAAAATAAAATGTATGTTTTCCTAAATGCGCAATATAAAAAATTTGTAATAAAAACACTGTATAGTAAT

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FIGURE 110

MDFLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGEICGPNKCKCHPGYAGKTCNQDLNECGLKPRPKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRCTCDVDECATGRASCPFRQC
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDGTGNNNWIPDVGSTWPPKTPYIPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTLRTPLPTTPTPTTGLTTIAPAASTPPGGITVDN
RVQTDPOKPRGDVFSVLVHSCNFDHGLCGWIREKDNLDLHWEPIRDPAGGQYLTVSAAKAPGG
KAARLVLPGLRMLHSGDLCLSPFRHKVTGLHSGTLQVVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

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FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCTTTAGATTGTGA
AATGTGGCTCAAGGCTTTACACACTTTCTCTTTCTTTGCAACAGGTGCTTGTCTCGGGGCTGA
 AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTTACCTACCCGTC
 CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA
 CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACC
 AACACAAGTTCAACATGATGCCACCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTT
 GATGAAGGCCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAACCTCTATCTGCCAGTCA
 GAAGATACAAGTCACGGTTGATGATCCTGTGCACAAGCCAGTGGTGCAGATTATCCTCCCT
 CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGCACTCGG
 CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
 TCCCCAAAACAATACCCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
 GCCTGGTGAGGAACCTGTGTCAGTGAATGGAAAGTGATATCATTATGCCCATCATATATTAT
 GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAAGTAGGGGAAGTGTTTACTGT
 TGACCTTGAGAGGCCATCCTATTGTATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
 CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAAGCATGGGCCTCGCTTAGAAGTT
 GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
 CGGCAGGCAAGATGAAACTCATTTCACAGTTATCATCACTCCGTAGGACTGGAGAAGCTTG
 CACAGAAAGGAAAAATCATTGTGCACCTTTAGCAAGTATAACTGGAATATCACTATTTTGTATT
 ATATCCATGTGTCTTCTCTTCCATGGAAAAAATATCAACCCACAAAGTTATAAAACAGAA
 ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACTTTTCAGGCCATGAAGATG
 CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGG
 ATTCGAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT
 GTATGAAGTTATTACGACATCCCTGCCAGCAGCAAGACCATCCAGAGTGA**ACT**TTTCATGG
 GCTAAACAGTACATTCGAGTGAAATCTGAAGAAACATTTTAAAGAAAAACAGTGGAAAAAGT
 ATATTAACTGGAATCAGTGAAGAAACAGGACCACACCTCTTACTCATTATTCTTTTACAA
 TGCAGAATAGAGGCATTTATGCAAAATGAACTGCAGGTTTTCAGCATATACAAATGTCTT
 GTGCAACAGAAAAACATGTTGGGGAATATTCCTCAGTGGAGAGTCTGTTCTCATGCTGACGG
 GGAGAACGAAAGTGACAGGGGTTTCTCATAAGTTTTGTATGAAATATCTCTACAAACCTCA
 ATTAGTTCTACTCTACATTTCACTATCATCAACACTGAGACTATCCTGTCTCACTACAA
 TGTGGAAACTTTACATTGTTTCGATTTTTCAGCAGACTTGTGTTTATTAATTTTATTAGTG
 TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTTGTACAA
 CAAAGTAATAAGGATGGTTGTCAAAAAACAAACTATGCCTTCTCTTTTTTTTCAATCACC
 AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTTA
 TTTTTTTCAGGAAAGATGGATTCAAATAAATTATTCGTTTTTGCTTTTAAAAA

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FIGURE 112

MWLKVFTTFLSFATGACSGLVKTVPSHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVVPDLEYQHKFTMPPNASLLINPLQFPDEGNYIVKVNIOGNGTLSASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPFVSEMESDIIMPIIYYGPGYGLQVNSDKGLKVGVEFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTM DYVCCAYNNIT
GRQDETHFTVITTSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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FIGURE 113

GCAAGCGGCGAAATGCGGCCCTCCGGGAGTCTTGCAGTTCGCCCTGGCAGTCTCTGGTGTCTGTT
 GCTTTGGGGTGCTCCCTGGAGCGCACGGGCGGGCGAGCAACGTTTCGGGTATCACGGACGAGA
 ACTGGAGAGAACTCTCTGGAAGGAGACTGGATGATAGAATTTTATGCCCGTGGTGCCCTGCT
 TGTCAAAATCTTCAACCGGAATGGGAAAGTTTGTCTGAATGGGAGAAGATCTTGAGGTTAA
 TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC
 TTCCTACTATTTATCATTTGTAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
 AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGCCCGTTTCATCATG
 GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACCTCTTTCAGCTATCTATGTGGA
 TCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT
 GTTTTTGTCTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC
 AGATTGCCTTTGTCCCTCAAAAAGGCGCAGACCAAGCCATACCCATACCCCTTCAAAAAAAT
 TATTATCAGAATCTGCACAACCTTTGAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
 GATGTTTCAGAAGAAGAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTTCACAGAATGC
 CATAAAGACAACGCTCTCTGGGTCCATCATTTGGCCACAGATAAATCCTAGTTAAATTTTATAG
 TTATCTTAATATTATGATTTTGATAAAACAGAAGATTGATCATTTTGTGTTGGTTGAAGTG
 AACTGTGACTTTTTTGAATATTGACAGGTTTCAGTCTAGATTGTCTATTAAATTGAAGAGTCTA
 CATTCAGAACATAAAAGCAGGTATACAAAGTTTGAATATGATTAAAGCAACAGTATGATG
 GTTTAAATAGTTCTCTAATTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTGT
 TTAATAATAACCTATTCTCAAGTCTGAGTTTGAATAATTACATTTCCCAAGTATTGCAATAT
 TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTCTCTG
 TTTCACTGTGTGAAAAAAGAAGATATTTCCATAAATGGGAAGTTTGGCCATTGTCTCAAG
 AAATGTGTATTTCAGTGACAATTTCTGGTCTTTTTAGAGGTATATCCAAAAATTTCTTGT
 ATTTTTAGGTTATGCAACTAATAAAAACTACCTTACATTAATTAATACAGTTTTCTACACA
 TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATT
 CAACAAAGTTTGATTTTCTCTGTATTTTTCTTACTTACTATGGGTTACATTTTTTATTTTT
 CAAATTTGGATGATAATTTCTTGGAAACATTTTTTATGTTTATAGTAAACAGTATTTTTTGT
 GTTTCAAACCTGAAGTTTACTGAGAGATCCATCAAATTGAACAACTCTGTTGTAATTTAAAT
 TTGGCCACTTTTTTTCAGATTTTACATCATTTCTGCTGAACCTCAACTTGAATTTGTTTTTT
 TTTCTTTTTGGATGTGAAGGTGAACATTTCTGATTTTTGTCTGATGTGAAAAAGCCTTGGTA
 TTTTACATTTTGAATAATCAAAGAAGCTTAATATAAAAGTTTGCATTTCTACTCAGGAAAAAG
 CATCTTCTGTATATGCTTAAATGTATTTTTGTCTCATATACAGAAAGTTCTTAATTGAT
 TTTACAGCTCTGAATGCTTGATGTTTTAAAAATAAATCAATTTTTATATTTTTTAAAGACAA
 ACTTCATATTATCCTGTGTTCTTTCTTGACTGGTAAATATTGTGTGGGATTTTCACAGGTAAAA
 GTCACTAGGATGGAACATTTTAGTGATTTTTTACTCCTTAAAGAGCTAGAAATACATAGTTTT
 CACCTTAAAGAAGGGGAAAAATCATAAATCAATGAATCACTGACCATTACGTAGTAGAC
 AATTTCTGTAATGTCCCCTTCTTCTAGGCTCTGTGTGCTGTGAATCCATTAGATTTACAG
 TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAAAATATTGTACCATT
 AAAGAGTTTGGATGTGTAACCTGTGATGCCTTAGAAAAATATCCTAAGCACAAATAAACCT
 TTCTAACCACTTCATTAAGCTGAAAAAATAAAAAAAAAA

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FIGURE 114

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFI SDK EWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEAEDEEDVSE
EEAESKEGTNKDFPQNAIQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT
 CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCCGATTGGAAGAGCGGG
 AAGGTCCTGGCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC
 ATTGCTGATGGCCTGGTTTGGTGTCTTGAGCTGTGTGCAGGCCGAATTCTTACCTCTATTG
 GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
 CTTGTGGAGGAAGCCAAGCTTTCCAAGATTAAAGAGCTGGGCCAACAAATGGAAGCCTTGAC
 TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCCTGTGAATGCCTACAAACTGG
 TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
 GGTTTTATCGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCACTGATGAGGACGAGATAGG
 AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA
 GAGGGGAACCTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
 GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT
 AAAGCAGCTTGATGCCGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
 GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTACCCCGCCGCTGCTC
 TCCCTTGACCCAAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA
 GGAAGAGAGAGAAAAACGTTAACAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCA
 TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGGGG
 GAGGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA
 CAGGGCCCCACAGCTGCTCATTGCCCTTCAAAGAGGAGGACGAGTGGGACAGCCGCACA
 TCGTCAGGTACTACGATGTCATGTCTGATGAGGAATCGAGAGGATCAAGGAGATCGCAAAA
 CCTAAACTTGCACGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCCCTCACTGTGCGCAGCTA
 CCGGGTTTCAAAAAGCTCCTGGCTAGAGGAAGATGATGACCCCTGTTGTGGCCCGAGTAAATC
 GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAA
 TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGCGACCTTTTGACAGCG
 CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGTGTAGAAGCTG
 GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG
 TTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCTTGGCCC
 TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT
 TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTTCTGTCTCTCCCTTCTCTGGTC
 CTTCAAGCCATGTCAACGTGCAGACACCTTTGTATGTTCCCTTGTATGTTCCCTATCAGGCT
 GATTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGCGCACTCCTGT
 GTGACTGAAGTCCCAGCCCTTCCATTGAGCCTGTGCCATCCCTGGCCCCCAAGGCTAGGATCA
 AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCTAGCAAGGTGCTTTGTACCTCAGGTGTT
 TTAGGTGTGAGATGTTTCAAGTAAACAAAGTTCTGATACCTTGTGTTTACATGTTGTTTTAT
 GGCATTTCTATCTATTGTGGCTTTACCAAAAAATAAATGTCCCTACCAGAAAAA

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FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFP
TDEDEIGAALKALMRLQDITYRLDPGTISRGE LPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPDYLPEDVYESLCRGEVGLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEEDWDSPHIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNRMMQHITGLTVKTAELLQVANYGVGGQYEPHDFDS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEVDYR
TRHAACPVLVGCKVSNKWFHERGQEFRLPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTTCTCTCTTTTATGTGGAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATTGT
 TTCACTTTATACCGTTTTTGGCTGGGGGTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAGAGGATTGTGA
 AGACAGGACAATCTTTTGGGGATGCTGGTCTTGGAGCCAGCGGGCTTGGCTGTCTTGGCTCATTGACCC
 CAGGTCTCTGGTTAAAACTGAAAGCCTACTACTGGCCTGGTGGCCATCAATCTCATTGATCCTTGAGGCTGTGCC
 CCTGGGGCACCCACCTGGCAGGGCTTACCACCTGCGACTGAGCTCCTGTGGCTCTGCTGGCGCCAGGCTTC
 CCCTCATCTTAGGGCTGTCTCTGGGGTGCAGCCTGAGCCTCCTGCGGGTTTCTGGATCCAGGGGAGGGAGAG
 ATCCTCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTTCAGAGCTCGGCTAGACCAAAGTG
 ATGAAGACTTCAAACCCCGATTGTCCCCTACTACAGGGACCCCAAGAGCCTACAGAAGGTGCTCAGGACTC
 GGTACATCCAGACAGAGCTGGGCTCCGTGAGCGGTTGCTGGTGGCTGTCTGACCTCCCGAGCTACACTGTCCA
 CTTTGGCCGTGGCTGTGAACCGTACGGTGGCCCATCACTTCTCGGTTACTTCACTTCACTGGGCAGCGGGGG
 CCGGGCTCCAGCAGGGATCAGGTTGGTGTCTCATGGGGATGAGCGGCCCGCTGGCTCATGTACAGACACCTGC
 GCCACCTTCAACACACCTTTGGGGCCGACTACGACTGGTCTTCTCATGAGGATGACACATATGTGACAGGCC
 CCGCCTTGGCAGCCCTTGTCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGGACAGAGGATTCATTG
 GCGCAGCGCAGCGGCCGGTACTGTCTAGGGGGCTTTGGCTACCTGTGTGTCAGGAGTCTCCTGCTTCGTCTGC
 GGCCAGTCTGATGGCTGCCGAGGAGACATTCTCAGTGCCCTGCTGACGAGTGGCTTGGACGCTGCCTCATTTG
 ACTCTCTGGGCTCGGCTGTCTCACAGCACAGGGGACAGTATCGCTCATTTGAACTGGCCAAAATAGGG
 ACCCTGAGAGAGGAGGGAGCTCGGCTTTCTGAGTGCCTTCCGCGTGACCCCTGTCTCCGAAGGTACCTCATGT
 ACCGGCTCCACAAACGCTTCAGCGCTCTGAGATTGGAGCGGCTTACAGTGAAATAGAACAACTGCAGGCTCAGA
 TCCGGAACCTGACCGTGCTGACCCCCGAAGGGAGGACAGGCTGAGCTGGCTGATCGTTGGAGATCGCTCCGCTGCTCTTCA
 CACCACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTACAGAGCAGCAGCTTCTCTCTGTGCGAGTGGGG
 CTCCCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGAGCTGGGTGATCGTTGGAGATCGCTCCCTGGAGCAGCTCA
 ATCGGCGCTCATGACCCCGCTGGCGCTCCAGAAGCAGCGACTGCTCAAAGCTATCGGCGCTTCGACCCAGCAC
 GGGCATGAGTACACCTCGGACCTGCTGTGGAATGTGTGACACAGGCTGGGACCGCGGCGGCTGGCTCGCA
 GGGTCAGCTGCTGCGGCCACTGAGCCGGGTGGAAATCTACCTATGCCCTATGTCTACTGAGGCCACCGAGTGC
 AGCTGGTGTGCCACTCTGTGGGTGAAGCTGCTGACGCCCGGCTTTCTCGAGGCGTTTGCAGCCCAATGTCC
 TGGAGCCACGAGAACATGCATTGCTCACCCTGTGTGCTGCTACGGGCCACGAGAAGGTGGCCGTGGACACTCTCT
 TCTTCTTACACCGTGTGGACAAGGCTGGGGCCGAAGTCTCAACCGCTGTGCGATGAATGCCATCTCTGGCT
 GGCAGGCTCTTCTTCAGTCCATTTCCAGGAGTTCAATCTGGCTGTACCAACAGAGATCACCCCCAGGGCCCC
 CGGGGGCTGGCCCTGACCCCCCTCCCTCTCTGGTGTGACCCCTCCCGGGGGGCTCCTATAGGGGGGAGATTG
 ACCGGCAGGCTTCTGCGGAGGGCTGCTTCTACACGCTGACTACTGGCGGCCGAGGCCCGCTGGCAGGTGAAC
 TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGGCTGGAGGTGATGGAATGTTTCTCCGGTCTCAGGGCTCC
 ACTCTTTTGGGGCTAGAGCCAGGGCTGGTGAGAGTTCTCCCTGCGACTGAGGCCACCGCTCAGTGAAG
 AACTCTACACCGCTGCGGCTCAGCAACTGGAGGGGCTAGGGGGCCGTGCCAGCTGGCTATGGCTCTCTTTG
 AGCAGGAGCAGGCCAATAGCACTTAGCCCGCTGGGGGCCCTAACTCATTAATCTTTTGTCTGCTGCCAGCC
 CCAGGAAGGCAAGCAAGATGTTGGACAGATAGAGAATGTTGCTGTATTTTAAATATGAAATGTTATTAA
 ACATGCTCTTCTGCC

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FIGURE 118

MRLSSLLALLRPALPLIILGLSLGCSLSLLRVSWIQEGEGEDPCVEAVGERGGPQNPDSSRARLD
QSDDEFKPRIVPYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVSHGDERPAWLMSETLRHLHTHFGADYDWFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRLLLLRLRPHLDGCRG
DILSARPDDEWLGRCLIDSLGVGCVSQHQQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELEBRAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCP LQGASRADVGDALETALEQLNRRYQPRLRFQKQRLNLNGYR
RFDPPARGMEYTLDDLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVLVPLLL
VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLNRCRMNAISGWQAFPP
VHFQEFNPALSPQRSPPGPPGAGDPSPSPGADPSRGAPIGGRFDROASAEGCFYNADYLAA
RARLAGELAGQEEEEALEGLEVMVDVFLRFSGHLHFRAVEPGLVQKFSRLDCSPRLSEELYHR
CRLSNLEGLGGRAQLAMALFEQEQA NST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAAATTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTGAGTATACTGTATTATCCTTGTAAACC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTGTGAGTCAATTATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAAGCTTACAAATACGCCCTTTGATAAGTATAGAGACCAATACAACTG
GTTCTTCTCTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAC
AGCTAGCAGTTTGCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAATCTGTTGGGCTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTGTTGAGATATGGCTGTACTTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGCATTGGGCATATTTTCAAT
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACACATATCCAA
TACAGCTGTATGTTTCTTTTCTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTCTTTTAAACACATGAACATTGTAAATG
TGTGGAAGAAGTGTTTTAAGAATAATAATTTGCAAATAAACTATTAATAAATATTATAT
GTGATAAAATCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTGTCTGATTGGTT
AAAAATTTTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACCTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT
AAGCCTCCCAAGTTCCAAATGGATTTCCTTCTCAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISED
LSKSFVRVYCIILVKPKDVSLLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMR
AYKYAFDKYRDQYNWFFLARPTTFAI IENLKYFLKDDPSQPFYLGHTIKSGDLEYVGM
IVLSVESMKRLNSLLNIPEKCPQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDV
KSVGLSIIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMYGVYRLRAFGHIFNDALV
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAAGAGAGGGAGGGAGAG
 AAAAAAGAGAGAGAGAGAGAAAACAAAAACCAAAGAGAGAGAAAAAATGAATTCATCTAAATCAT
 CTGAAACACAATGCACAGAGAGAGGGATGCTTCTCTTCCCAAATGTTCTTATGGACTGTTGCT
 GGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTTCGCAT
 CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTACAGAGCTCTCCTGCT
 ACAATTATGGATCAGGTTCAAGTCAAGAATTGTTGTCCATTGAACTGGGAATATTTTCAATCC
 AGCTGCTACTTCTTTTCTACTGACACCATTTCCTGGGCGTTAAGTTTAAAGAACTGCTCAGC
 CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCCTACAAGA
 AACCTAAAATGAGAGAGTTTTTTATGGAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA
 TGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA
 CATAGCTACCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATTGGA
 ATGATGTAACCTGTTTCTCAATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTG
 AACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACCTCAAATGTGTAAGAAGGAAGAGCA
 AGAACATGGCCACACCCACCGCCCCACACGAGAAATTTGTGCGCTGAACTTCAAAGGACTTC
 ATAAGTATTTGTTACTCTGATACAAATAAAAATAAGTAGTTTTAAATGTTAAAAA
 AA
 AAAAA

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Signal sequence:

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCTCAGCAACCCCTCGACATGCGCGCTGAGCGGGCCACCCGCGAC
 TCCGGCTCTCGCGCTCGGCTGCTGACTTCTTCTCGTGTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC
 TCAAACTCCAGAACTCGAACCCAGTCAGTGGTACAGGAATTTGAAAGTGTGGAACTGTCTTGTCATCATACGGATTCCG
 AGACAAGTGACCCAGGATCGAGTGGGAAGAAATTCAGATGAAACAAACCATATGTGTCTTTTGACAAACAAAA
 TTCAGGAGGACTTGGCGGGTCTGTGCAGAAATCTGGGGAAGACATCCCTGAAGATCTGGAACTGTGAACAGGGAG
 ACTCAGCCCTTTATCGCTGTGAGGTCTGTCTCGAAATGACCGCAAGGAAATGTAGAGATTGTGATCGAGTTAA
 CTGTGCTCAAGTGAAGCCAGTGAACCCCTGTCTGTAGAGTGCAGAGGCTGTACAGTAGGCAAGATGGCAACACTGC
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03905532.071301

FIGURE 124

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RK
EIDEIVIELTVQVKPVTVPVCRVPKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDS
RA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEYVDLNI
GGIIG
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGD
FRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267